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RESULT 15  
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LOCUS AF465211 1768 bp DNA circular VRL 07-FEB-2002  
DEFINITION Porcine circovirus type 2 strain SC, complete genome.  
ACCESSION AF465211  
VERSION AF465211.1 GI:18448942  
KEYWORDS  
SOURCE porcine circovirus type 2.  
ORGANISM porcine circovirus type 2  
REFERENCE Viruses; ssDNA viruses; Circoviridae; Circovirus.  
1 (bases 1 to 1768)  
AUTHORS Wang,C., Pan,C.H., Huang,C.C., Huang,T.S., Jong,M.H., Lin,S.Y. and Lai,S.S.  
TITLE Complete nucleotide sequences of porcine circovirus type 2 isolated in pigs with various clinical syndromes  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1768)  
AUTHORS Wang,C., Pan,C.H., Huang,C.C., Huang,T.S., Jong,M.H., Lin,S.Y. and Lai,S.S.  
TITLE Direct Submission  
JOURNAL Submitted (02-JAN-2002) Hog Cholera Department, National Institute for Animal Health, 376 Chung-cheng Road, Tamsui, Taipei 25101, Taiwan  
FEATURES  
source Location/Qualifiers  
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Query Match 88.8%; Score 623.6; DB 14; Length 1768;  
Best Local Similarity 93.0%; Pred. No. 5.6e-168;  
Matches 653; Conservative 0; Mismatches 49; Indels 0; Gaps 0;  
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Search completed: May 18, 2003, 11:41:48  
Job time : 2030 secs

REFERENCE 1 Viruses; ssDNA viruses; Circoviridae; Circovirus.  
1 (bases 1 to 1767)  
AUTHORS Hutet,E. and Albina,E.  
TITLE Circovirus sequences related to piglet weight loss disease (pwd)  
JOURNAL Patent: WO 9929871-A 10 17-JUN-1999;  
HUTET EVELYNE (FR); ALBINA EMMANUEL (FR)  
FEATURES  
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154 AAAAAATGGCATCTTCAACACCCCGCTCTCCCGCACCTTCGGATATACTGTCAAGCGAAC 213  
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214 ACAGTCAGAACGCCCTCCTGGCGGTTGACATGATGAGATTCAATTAATGACTTTCTT 273  
QY 241 CCCCCAGGAGGGGGTCAAAACCCCGCTCTGTGCCCTTTGAATACTACAGAATAAGAAAG 300  
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274 CCCCCAGGAGGGGGTCAAAACCCCGCTCTGTGCCCTTTGAATACTACAGAATAAGAAAG 333  
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454 TATGTAACACTACTCCTCCGCCATACCATACCAGCCCTTCTCCTACCACCTCCCGGTAC 513  
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514 TTTACCCCCAAACCTGTCTCTAGATTTCACATATTGATTACTTCCAAACCAACAACAAAGA 573  
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Db |  
574 AACCAGCTGTGGCTGAGACTACAAACTGCTGGAAATGTAGACCACGTAGGCCTCGGCAC 633  
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RESULT 4  
AF201311/c 1767 bp DNA circular VRL 23-FEB-2000  
LOCUS Porcine circovirus type 2 isolate FRA3, complete genome.  
DEFINITION AF201311  
ACCESSION AF201311  
VERSION AF201311.1 GI:7021361

KEYWORDS porcine circovirus type 2.  
SOURCE porcine circovirus type 2  
ORGANISM Viruses; ssDNA viruses; Circoviridae; Circovirus.  
REFERENCE 1 (bases 1 to 1767)  
AUTHORS Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A., Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.  
TITLE Characterisation of PCV-2 isolates from Spain, Germany and France  
JOURNAL Virus Res. 66 (1), 65-77 (2000)  
MEDLINE 20120936  
PUBMED 10653918  
REFERENCE 2 (bases 1 to 1767)  
AUTHORS Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A., Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.  
TITLE Direct Submission  
JOURNAL Submitted (03-NOV-1999) p24, Robert Koch Institut, Nordufer 20, Berlin 13353, Germany  
FEATURES  
Location/Qualifiers  
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BASE COUNT 449 a 361 c 498 g 459 t  
ORIGIN  
Query Match 99.5%; Score 698.8; DB 14; Length 1767;  
Best Local Similarity 99.7%; Pred. No. 1.4e-189;  
Matches 700; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ATGACGTATCCAAGGAGCGGTTACCGAAGAAGACACCGCCCCCGCAGCCATCTTGGC 60  
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Db |  
677 CAGATCCTCCGCCCGCCCTCGGCTCGTCCACCCCGCCACCGTTACCGCTGGAGAAG 618  
QY 121 AAAAAATGGCATCTTCAACACCCCGCTCTCCCGCACCTTCGGATATACTGTCAAGCGAAC 180  
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617 AAAAAATGGCATCTTCAACACCCCGCTCTCCCGCACCTTCGGATATACTGTCAAGCGAAC 558  
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Db 557 ACAGTCAGAACGCCCTCCTGGCGGTGGACATGATGAGATTCAATATTAATGACTTTCTT 498

QY 241 CCCCCAGGAGGGGTCAAACCCCGCTCTGTGCCCTTTGAATACTACAGAATAAGAAAG 300

Db 497 CCCCCAGGAGGGGTCAAACCCCGCTCTGTGCCCTTTGAATACTACAGAATAAGAAAG 438

QY 301 GTTAAGGTTGAATCTGGCCCTGCTCCCGGATCACCCAGGGTGACAGGGGAGTGGGCTCC 360

Db 437 GTTAAGGTTGAATCTGGCCCTGCTCCCGGATCACCCAGGGTGACAGGGGAGTGGGCTCC 378

QY 361 AGTGCTGTTATTTTAGATGATAACTTTGTAAACAAAGGCCACAGCCCTCACCTATGACCCC 420

Db 377 AGTGCTGTTATTTTAGATGATAACTTTGTAAACAAAGGCCACAGCCCTCACCTATGACCCC 318

QY 421 TATGTAAACTACTCCTCCCGCATACCATACCCAGCCCTTCTCTACCACCTCCCGGTAC 480

Db 317 TATGTAAACTACTCCTCCCGCATACCATACCCAGCCCTTCTCTACCACCTCCCGGTAC 258

QY 481 TTTACCCCCAAACCTGTCTAGATTTCACTATTGATTACTTCCAACCAACAAACAAAGA 540

Db 257 TTTACCCCCAAACCTGTCTAGATTTCACTATTGATTACTTCCAACCAACAAACAAAGA 198

QY 541 AACCAGCTGTGGCTGAGACTACAAACTGCTGGAAATGTAGACCACGTAGGCCCTCGGCAC 600

Db 197 AACCAGCTGTGGCTGAGACTACAAACTGCTGGAAATGTAGACCACGTAGGCCCTCGGCAC 138

QY 601 GCGTTCGAAACACGTATATACGACCAGGAATACAATATCCGTGTAAACCATGTATGTACAA 660

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Db 77 TTCAGAGAAATTTAATTTTAAAGACCCCCCACTTAACCCCTTAA 36

RESULT 5

AY122275/c

LOCUS

DEFINITION Porcine circovirus type 2 isolate kaozhai, complete genome.

ACCESSION AY122275

VERSION AY122275.1 GI:22121723

KEYWORDS

SOURCE Porcine circovirus type 2.

ORGANISM Porcine circovirus type 2

REFERENCE 1 (bases 1 to 1767)

AUTHORS Cui,S.J., Li,Y., Li,J.W., Jin,H. and Tong,G.Z.

TITLE Isolation and Identification of Porcine Circovirus Type 2

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1767)

AUTHORS Cui,S.J., Li,Y., Li,J.W., Jin,H. and Tong,G.Z.

TITLE Direct Submission

JOURNAL Submitted (14-JUN-2002) Harbin Veterinary Research Institute of CAAS, No. 427, Maduanjie, Nangang Distict, Harbin, Heilongjiang 150001, P. R. China

FEATURES

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BASE COUNT 449 a 360 c 498 g 459 t 1 others

ORIGIN

Query Match 99.5%; Score 698.8; DB 14; Length 1767;

Best Local Similarity 99.7%; Pred. No. 1.4e-189;

Matches 700; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACGTATCCAAGGAGGCGTTACCGAAGAAGACACACCGCCCCCGCAGCCATCTTGGC 60

Db 737 ATGACGTATCCAAGGAGGCGTTACCGAAGAAGACACCGCCCCCGCAGCCATCTTGGC 678

QY 61 CAGATCCTCCGCGCGCCCTCGTCTGCCACCCCGCCACCGCTTACCGCTGGAGAAG 120

Db 677 CAGATCCTCCGCGCGCCCTCGTCTGCCACCCCGCCACCGCTTACCGCTGGAGAAG 618

QY 121 AAAATGGCATCTTCAACACACCCCGCTCTCCCGCACCTTCGGATATACTGTCAAGCGAAC 180

Db 617 AAAATGGCATCTTCAACACACCCCGCTCTCCCGCACCTTCGGATATACTGTCAAGCGAAC 558

QY 181 ACAGTCAGAACCGCCCTCCTGGCGGTGGACATGATGAGATTCAATATTAATGACTTTCTT 240

Db 557 ACAGTCAGAACCGCCCTCCTGGCGGTGGACATGATGAGATTCAATATTAATGACTTTCTT 498

QY 241 CCCCCAGGAGGGGTCAAACCCCGCTCTGTGCCCTTTGAATACTACAGAATAAGAAAG 300

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Db 437 GTTAAGGTTGAATCTGGCCCTGCTCCCGGATCACCCAGGGTGACAGGGGAGTGGGCTCC 378

QY 361 AGTGCTGTTATTTTAGATGATAACTTTGTAAACAAAGGCCACAGCCCTCACCTATGACCCC 420

Db 377 AGTGCTGTTATTTTAGATGATAACTTTGTAAACAAAGGCCACAGCCCTCACCTATGACCCC 318

QY 421 TATGTAAACTACTCCTCCCGCATACCATACCCAGCCCTTCTCTACCACCTCCCGGTAC 480

Db 317 TATGTAAACTACTCCTCCCGCATACCATACCCAGCCCTTCTCTACCACCTCCCGGTAC 258

QY 481 TTTACCCCCAAACCTGTCTAGATTTCACTATTGATTACTTCCAACCAACAAACAAAGA 540

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Db 197 AACCAGCTGTGGCTGAGACTACAAACTGCTGGAAATGTAGACCACGTAGGCCCTCGGCAC 138

QY 601 GCGTTCGAAACACGTATATACGACCAGGAATACAATATCCGTGTAAACCATGTATGTACAA 660

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RESULT 6

AF201897/c

LOCUS

AF201897 1767 bp DNA circular VRL 20-DEC-2000



DEFINITION Porcine circovirus type 2, complete genome.  
ACCESSION AF201897  
VERSION AF201897.1 GI:11907587  
KEYWORDS porcine circovirus type 2.  
SOURCE porcine circovirus type 2  
ORGANISM Viruses; ssDNA viruses; Circoviridae; Circovirus.  
REFERENCE 1 (bases 1 to 1767)  
AUTHORS Wellenberg,G.J., Pesch,S., Berndsen,F.W., Steverink,P.J.G.M., Hunneman,W., Van der Vorst,T.J.K., Peperkamp,N.H.M.T., Ohlinger,V.F., Schippers,R., Van Oirschot,J.T. and de Jong,M.F.  
TITLE Isolation and characterization of porcine circovirus type 2 from pigs showing signs of post-weaning multisystemic wasting syndrome in The Netherlands  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1767)  
AUTHORS Pesch,S. and Ohlinger,V.F.  
TITLE Direct Submission  
JOURNAL Submitted (04-NOV-1999) Virology and Molecular Epidemiology, BioScreen European Veterinary Disease Management Center GmbH, 11 Mendelstr., Muenster, NRW 48149, Germany  
FEATURES  
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/db\_xref="GI:11907595"  
/translation="MDIDHTVSDHPRAASHKSHQ"  
complement(989..1033)  
/gene="ORF11"  
complement(989..1033)  
/gene="ORF11"  
/note="1.8 kDa"  
/codon\_start=1  
/evidence=not\_experimental  
/product="ORF11"  
/protein\_id="AAG41230.1"  
/db\_xref="GI:11907592"  
/translation="MNNKNHYEVIKKTQ"  
complement(1033..1734)  
/gene="ORF2"  
complement(1033..1734)  
/gene="ORF2"  
/note="27.8 kDa"  
/codon\_start=1  
/evidence=not\_experimental  
/product="ORF2"  
/protein\_id="AAG41227.1"  
/db\_xref="GI:11907589"  
/translation="MTYPRRRYRRRRHRRPSHLGQILRRRPWLVPRHRYRWRKNGI FNTRLRTEGYTVKRTTVTPSPWAVDMRFNINDELPPGGGNSPRSVFYYRIRKVK VEFWPCSPITQGDVGSSAVILDDNEVTKATALTYDPYVNYSSRHTITQPFYSHSRY FTPKPVLDSTIDYFQPNKNRNLWLRLQTAGNVHDVGLGTAFENSIYDQEYNIRVTMY VQFREPNLKDPPPLNP"  
complement(1521..1610)  
/gene="ORF6"  
complement(1521..1610)  
/gene="ORF6"  
/note="3.1 kDa"  
/codon\_start=1  
/evidence=not\_experimental  
/product="ORF6"  
/protein\_id="AAG41231.1"  
/db\_xref="GI:11907593"  
/translation="MASSTPASPADPSDILSSEPQSERPPGRWT"  
1523..1630  
/gene="ORF10"  
1523..1630  
/gene="ORF10"  
/note="4.1 kDa"  
/codon\_start=1  
/evidence=not\_experimental  
/product="ORF10"  
/protein\_id="AAG41235.1"  
/db\_xref="GI:11907597"  
/translation="MSTAQEGVLTVVRLTVYPKVRERRVLKMPFFLLQR"  
1681..1740  
/gene="ORF7"  
1681..1740  
/gene="ORF7"  
/note="1.9 kDa"  
/codon\_start=1  
/evidence=not\_experimental  
/product="ORF7"

/protein\_id="AAG41232.1"  
/db\_xref="GI:11907594"  
/translation="MAAGAVSSSPVTPPWIRHI"  
BASE COUNT 448 a 361 c 500 g 458 t  
ORIGIN

Query Match 98.4%; Score 690.8; DB 14; Length 1767;  
Best Local Similarity 99.0%; Pred. No. 2.7e-187;  
Matches 695; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGACGTATCCAAGGAGGCGTTACCGAAGAAGAAGACACCGCCCGCAGCCATCTTGGC 60  
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Db 1734 ATGACGTATCCAAGGAGGCGTTACCGGAGAAGAAGACACCGCCCGCAGCCATCTTGGC 1675  
QY 61 CAGATCCTCCGCCCGCCCTGGCTCGTCCACCCCGCCACCGTTACCGCTGGAGAAG 120  
|||||  
Db 1674 CAGATCCTCCGCCCGCCCTGGCTCGTCCACCCCGCCACCGTTACCGCTGGAGAAG 1615  
QY 121 AAAAATGGCATCTTCAACACCCCGCCTCTCCCGCACCTTCGGATATACTGTCAAGCGAACC 180  
|||||  
Db 1614 AAAAATGGCATCTTCAACACCCCGCCTCTCCCGCACCTTCGGATATACTGTCAAGCGAACC 1555  
QY 181 ACAGTCAGAACGCCCTCCTGGGGGTGGACATGATGAGATTCAATATTAATGACTTTCTT 240  
|||||  
Db 1554 ACAGTCAGAACGCCCTCCTGGGGGTGGACATGATGAGATTCAATATTAATGACTTTCTT 1495  
QY 241 CCCCCAGGAGGGGTCAAACCCCGCTCTGTGCCCTTTGAATACTACAGAATAAGAAAG 300  
|||||  
Db 1494 CCCCCAGGAGGGGTCAAACCCCGCTCTGTGCCCTTTGAATACTACAGAATAAGAAAG 1435  
QY 301 GTTAAGGTTGAATTCTGGCCCTGCTCCCGGATCACCCAGGCTGACAGGGGAGTGGGCTCC 360  
|||||  
Db 1434 GTTAAGGTTGAATTCTGGCCCTGCTCCCGGATCACCCAGGCTGACAGGGGAGTGGGCTCC 1375  
QY 361 AGTGCTGTTATTTAGATGATAACTTTGTAACAAAGGCCACAGCCCTCACCTATGACCCC 420  
|||||  
Db 1374 AGTGCTGTTATTTAGATGATAACTTTGTAACAAAGGCCACAGCCCTCACCTATGACCCC 1315  
QY 421 TATGTAAACTACTCCTCCCGGCATACCATAACCCAGCCCTTCTCCTACCACCTCCCGGTAC 480  
|||||  
Db 1314 TATGTAAACTACTCCTCCCGGCATACCATAACCCAGCCCTTCTCCTACCACCTCCCGGTAC 1255  
QY 481 TTTACCCCCAAACCTGTCTAGATTTCACTATTGATTACTTCCAACCAACAAACAAAGA 540  
|||||  
Db 1254 TTTACCCCCAAACCTGTCTAGATTTCACTATTGATTACTTCCAACCAACAAACAAAGA 1195  
QY 541 AACCAGCTGTGGCTGAGACTACAAACTGCTGGAAATGTAGACCACGTAGGCCTCGGCAC 600  
|| |||||  
Db 1194 AATCAGCTGTGGCTGAGACTACAAACTGCTGGAAATGTAGACCACGTAGGCCTCGGCAC 1135  
QY 601 CGGTCGAAACAGTATATACGACCAGGAATACAATATCCGTGTAACCATGTATGTACAA 660  
|||||  
Db 1134 CGGTCGAAACAGTATATACGACCAGGAATACAATATCCGTGTAACCATGTATGTACAA 1075  
QY 661 TTCAGAGAAATTTAATTTTAAAGACCCCCCCTTAACCCCTTAA 702  
|||||  
Db 1074 TTCAGAGAAATTTAATCTTAAAGACCCCCCCTTAACCCCTTAA 1033

RESULT 7  
PCI293869/c  
LOCUS Porcine circovirus rep gene for replication-associated protein, isolate Imp.1147. 1766 bp DNA circular VRL 06-JUN-2001  
DEFINITION  
ACCESSION AJ293869  
VERSION AJ293869.1 GI:14330690  
KEYWORDS rep gene; replication-associated protein gene.  
SOURCE porcine circovirus.  
ORGANISM porcine circovirus  
Viruses; ssDNA viruses; Circoviridae; Circovirus.  
REFERENCE 1 (bases 1 to 1766)  
AUTHORS Meehan,B.M., McNeilly,F., McNair,I., Walker,I., Ellis,J.A., Krakowka,S. and Allan,G.M.

TITLE Isolation and characterization of porcine circovirus 2 from cases of sow abortion and porcine dermatitis and nephropathy syndrome  
JOURNAL Arch. Virol. 146 (4), 835-842 (2001)  
MEDLINE 21296605  
PUBMED 11402869  
REFERENCE 2 (bases 1 to 1766)  
AUTHORS Meehan,B.M., McNeilly,F., McNair,I., Walker,I., West,K., Ellis,J.A., Krakowka,S., Kennedy,S. and Allan,G.M.  
TITLE Isolation and characterization of porcine circovirus type 2 from cases of sow abortion and porcine dermatitis and nephropathy syndrome  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 1766)  
AUTHORS Meehan,B.M.  
TITLE Direct Submission  
JOURNAL Submitted (25-AUG-2000) Meehan B.M., Veterinary Science, The Queen's University of Belfast, Stormont, BT4 3SD, UNITED KINGDOM  
FEATURES  
source  
1..1766  
/organism="porcine circovirus"  
/virion  
/isolate="Imp.1147"  
/db\_xref="taxon:46221"  
/country="United Kingdom:UK"  
/note="PcV2 isolated from case of porcine dermatitis and nephropathy syndrome in the UK"  
59..1003  
/gene="rep"  
59..1003  
/gene="rep"  
/codon\_start=1  
/product="replication-associated protein"  
/protein\_id="CAC41085.1"  
/db\_xref="GI:14330691"  
/translation="MPSKKNGRSGPQPHKRWVFTLNNPSEDERKKIRDLPISLFDYFI VGEENEGRTPHLQGFANFVKQTFNKVKWYLGARCHIEKAKGTDOONKEYCSKEGN LLIECGAPRSQGRSDLSTAVSTLLESGLTVAEQHPVTFVRNFRGLAELLKVSQKM OKRDWKTNVHVIIVGPPCGKSKWAANFADPETTYWKPPRNKWDGYHGEVWVDDFY GWLPWDDLRLCDRYPLTVETKGGTVFPLARSILITSNQTPLEWYSSTAVPAVEALYR RITSLVFNKNATEQSTEEGGFVTLSPCPPEFYEINY"  
BASE COUNT 450 a 363 c 496 g 457 t  
ORIGIN

Query Match 97.3%; Score 682.8; DB 14; Length 1766;  
Best Local Similarity 98.3%; Pred. No. 5.5e-185;  
Matches 690; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ATGACGTATCCAAGGAGGCGTTACCGAAGAAGAAGACACCGCCCGCAGCCATCTTGGC 60  
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Db 1742 ATGACGTATCCAAGGAGGCGTTACCGGAGAAGAAGACACCGCCCGCAGCCATCTTGGC 1683  
QY 61 CAGATCCTCCGCCCGCCCTGGCTCGTCCACCCCGCCACCGTTACCGCTGGAGAAG 120  
|||||  
Db 1682 CAGATCCTCCGCCCGCCCTGGCTCGTCCACCCCGCCACCGTTACCGCTGGAGAAG 1623  
QY 121 AAAAATGGCATCTTCAACACCCCGCCTCTCCCGCACCTTCGGATATACTGTCAAGCGAACC 180  
|||||  
Db 1622 AAAAATGGCATCTTCAACACCCCGCCTCTCCCGCACCTTCGGATATACTGTCAAGCGAACC 1563  
QY 181 ACAGTCAGAACGCCCTCCTGGCGGTGGACATGATGAGATTCAATATTAATGACTTTCTT 240  
|||||  
Db 1562 ACAGTCAGAACGCCCTCCTGGCGGTGGACATGATGAGATTCAATATTAATGACTTTCTT 1503  
QY 241 CCCCCAGGAGGGGTCAAACCCCGCTCTGTGCCCTTTGAATACTACAGAATAAGAAAG 300  
|||||  
Db 1502 CCCCCAGGAGGGGTCAAACCCCGCTCTGTGCCCTTTGAATACTACAGAATAAGAAAG 1443  
QY 301 GTTAAGGTTGAATTTCTGGCCCTGCTCCCGCATCACCCAGGGTGACAGGGGAGTGGGCTCC 360  
|||||  
Db 1442 GTTAAGGTTGAATTTTGGCCCTGCTCCCGCATCACCCAGGGTGACAGGGGAGTGGGCTCC 1383  
QY 361 AGTGCTGTTATTTAGATGATAACTTTGTACAAAGGCCACAGCCCTCACCTATGACCCC 420  
|||||

Db 1382 AGTGCTGTTATTCTAGATGATAACTTTGTAAACAAGGCCACAGCCCTCACCTATGACCCC 1323

QY 421 TATGTAAACTACTCTCCCGCCATACCATACCCAGCCCTTCTCCTACCACTCCCGGTAC 480

Db 1322 TATGTAAACTACTCTCCCGCCATACCATACCCAGCCCTTCTCCTACCACTCCCGGTAC 1263

QY 481 TTTACCCCCAAACCTGTCTCTAGATTTTCACTATTGATTACTTCCAAACCAACAACAAGA 540

Db 1262 TTTACCCCCAAACCTGTCTCTAGATTTTCACTATTGATTACTTCCAAACCAACAACAAGA 1203

QY 541 AACCAGCTGTGGCTGAGACTACAAACTGCTGGAATGTAGACCACGTAGGCCTCGGCACT 600

Db 1202 AATCAGCTGTGGCTGAGACTACAAGCTGCTGGAATGTAGACCACGTAGGCCTCGGCACT 1143

QY 601 GCGTTCGAAACAGTATATACGACGAGGAATACAATATCCGTGTAACCATGTATGTACAA 660

Db 1142 GCGTTCGAAACAGTATATACGACGAGGAATACAATATCCGTGTAACCATGTATGTACAA 1083

QY 661 TTCAGAGAAATTTAATTTTAAAGACCCCCCTTAAACCCTTAA 702

Db 1082 TTCAGAGAAATTTAATCTTAAAGACCCCCCTTAAACCCTTAA 1041

RESULT 8

AY035820/c

LOCUS AY035820 1767 bp DNA circular VRL 13-JUN-2001

DEFINITION Porcine circovirus type 2, complete genome.

ACCESSION AY035820

VERSION AY035820.1 GI:14422165

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .1767

/organism="porcine circovirus type 2"

/db\_xref="taxon:85708"

/country="China"

/note="isolated from a pig with PMWS"

complement(join(1731. .1767,1. .92))

/note="ORF9"

/codon\_start=1

/evidence=not\_experimental

/product="unknown"

/protein\_id="AAK60470.1"

/db\_xref="GI:14422174"

/translation="MWLGASSILLARHVAAEVLPRCCRCRSALVILTAHFFRFQR"

join(1749. .1767,1. .13)

51. .995

/note="ORF1"

/codon\_start=1

/product="rep protein"

/protein\_id="AAK60462.1"

/db\_xref="GI:14422166"

/translation="MPSKKNRSGSQPHKRWVFTLNNPSEDERKKIRELPISLFDYFI

VGEEGNEGRTPHLOGFANFVKQTENKVKYFGARCHIEKAKGTDQONKEYCSKEGN

LLMECAQPSQQRSDLSSAVSTLSEGS�VTVAEQHPVTFVRNFRGLAELLKVSCKM

QKRDWKTNVHVIQPPCGGSKWAANFADPETTYWKP RNKWDGYHGEEVVIDDFY

GWLPWDDLRLCDRYPLTVEKTKGTVPLARSILITSQTPLEWYSSAVPAVEALYR

RITSLVFWKNATEQSTEEGGQFVTLSPPCPEFFYEINY"

117. .125

/note="glycosylation site"

816. .824

misc\_feature

misc\_feature

misc\_feature

polyA\_signal

CDS

/note="glycosylation site"

906. .914

/note="glycosylation site"

327. .332

complement(357. .671)

/note="ORF3"

/codon\_start=1

/product="unknown"

/protein\_id="AAK60464.1"

/db\_xref="GI:14422168"

/translation="MVTIPPLVSRWFPVCGFRVCKISSPEAFITTPRWPHNDVYIGLPI

TLLHPPAHFQKFSQPAEISDKRYRVLLCNHGQTTALQQGTHSTRQVTPLSLRSRSTL

HQ"

complement(386. .565)

/note="ORF4"

/codon\_start=1

/product="unknown"

/protein\_id="AAK60465.1"

/db\_xref="GI:14422169"

/translation="MTC TLVFQSRFCIFPLTEKSSASPRKFLTNTVNGCCSATVTRLPL

SNKVLTA LDRSLRCP"

complement(470. .478)

/note="glycosylation site"

complement(688. .753)

/note="ORF8"

/codon\_start=1

/evidence=not\_experimental

/product="unknown"

/protein\_id="AAK60469.1"

/db\_xref="GI:14422173"

/translation="MDIDHTVSDHPTAASHKSHQ"

983. .988

1016. .1105

/note="ORF5"

/codon\_start=1

/evidence=not\_experimental

/product="unknown"

/protein\_id="AAK60466.1"

/db\_xref="GI:14422170"

/translation="MVFIHGLSGSLRLNSLNTYMTVTRIL"

complement(1022. .1027)

complement(1030. .1734)

/note="ORF2"

/codon\_start=1

/product="capsid protein"

/protein\_id="AAK60463.1"

/db\_xref="GI:14422167"

/translation="MTYPRRRRRRRHRRSHLGOILRRRPWLVIHPRHRYWRRKNGI

FNTRLRSRTFGYTVKKTVRTPTPSWAVDMRMFNIDFLPPGGSNPLTPVFEYIRKVK

VEFWPCSPITQDGRGVGSTAVILDNDFVTKATALTYDPYVNYSSRHTITQPFYSHSRY

FTPKPVL DSTIDYFQPNKRNQLWRLQTSANVDHVGLGTAFENSIYDQDYNIRVTMY

VQREFNLKDPPLNPK"

complement(1300. .1311)

/note="glycosylation site"

complement(1521. .1610)

/note="ORF6"

/codon\_start=1

/evidence=not\_experimental

/product="unknown"

/protein\_id="AAK60467.1"

/db\_xref="GI:14422171"

/translation="MASSTPAS PAPSDILSRKPQSERPPGRWT"

1523. .1630

/note="ORF10"

/codon\_start=1

/evidence=not\_experimental

/product="unknown"

/protein\_id="AAK60471.1"

/db\_xref="GI:14422175"

/translation="MSTAQEGVLTVVFLTVYPKVRERRVLKMPFFLLQR"

1681. .1740

/note="ORF7"

/codon\_start=1

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CDS

misc\_feature

/evidence=not\_experimental

/product="unknown"

/protein\_id="AAK60468.1"

/db\_xref="GI:14422172"

/translation="MAAGAVSSSAETPPWIRHR"

455 a

363 c

498 g

451 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches 665; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY

1

ATGACGTATCCAAAGGAGCGTTACCGAAGAAGACACCGCCCGCAGCCATCTTGGC

60

Db

1734

ATGACGTATCCAAAGGAGCGTTCCGCAGACGACACCGCCCGCAGCCATCTTGGC

1675

QY

61

CAGATCCTCCGCCCGCCCTCGGCTCGTCCACCCCGCCACCGTTACCGCTGGAGAAGG

120

Db

1674

CAGATCCTCCGCCCGCCCTCGGCTCGTCCACCCCGCCACCGTTACCGCTGGAGAAGG

1615

QY

121

AAAAATGGCATCTTCAACACCCCGCCTCTCCCGCACCTCGGATATACTGTCAAGCGAACC

180

Db

1614

AAAAATGGCATCTTCAACACCCCGCCTCTCCCGCACCTTCGGATATACTGTCAAGAAAACC

1555

QY

181

ACAGTCAGAACGCCCTCCTGGCGGTGGACATGATGAGATTCAATATTAATGACTTTCTT

240

Db

1554

ACAGTCAGAACGCCCTCCTGGCGGTGGACATGATGAGATTAAATATTAACGATTTCCTT

1495

QY

241

CCCCCAGGAGGGGTCAAACCCCGCTCTGTGCCCTTTGAATACTACAGAATAAGAAAG

300

Db

1494

CCCCCAGGAGGGGTCAAACCCCGCTCACTGTGCCCTTTGAATACTACAGAATAAGAAAG

1435

QY

301

GTTAAGGTTGAATTCTGGCCCTGCTCCCGGATCACCCAGGGTGACAGGGGAGTGGGCTCC

360

Db

1434

GTTAAGGTTGAATTCTGGCCCTGCTCCCGGATCACCCAGGGTGACAGGGGAGTGGATCC

1375

QY

361

ACTGCTGTTATTTTAGATGATAACTTTGTAACAAAGGCCACAGCCCTCACCTATGACCCC

420

Db

1374

ACTGCTGTTATTTCTAGATGATAACTTTGTAACAAAGGCCACAGCCCTGACTTATGATCCC

1315

QY

421

TATGTAAACTACTCCTCCGCCATACCATAACCCAGCCCTTCTCCTACCACCTCCCGGTAC

480

Db

1314

TATGTAAACTACTCCTCCGCCATACCATAACCCAGCCCTTCTCCTACCACCTCCCGGTAC

1255

QY

481

TTTACCCCCAAACCTGTCTAGATTTCACTATTGATTACTTCAACACCAACAAACAAAGA

540

Db

1254

TTTACCCCCGAAACCTGTTCTTGATTCCACTATTGATTACTTCAACCAATAACAAAGG

1195

QY

541

AACCAGCTGTGGCTGAGACTACAAACTGCTGGAAATGTAGACCACGTAGGCCTCGGCAC

600

Db

1194

AATCAGCTTTGGCTGAGGCTACAAACCTCTGCAATGTGGACCACGTTAGGCCTCGGCAC

1135

QY

601

CGGTCGAAACACAGTATATACGACCAGGAATACAATATCCGTGTAAACCATGTATGTACAA

660

Db

1134

CGGTCGAAACACAGTATATACGACCAGGACTACAATATCCGTGTAAACCATGTATGTACAA

1075

QY

661

TTCAGAGAATTTAATTTAAAGACCCCCCTTAACCCCTTA

701

Db

1074

TTCAGAGAATTTAATCTTAAAGACCCCCCTTAACCCCTTA

1034

RESULT 9

AF201309/c

LOCUS

DEFINITION Porcine circovirus type 2 isolate SPA2, complete genome.

ACCESSION AF201309

VERSION AF201309.1 GI:7021355

KEYWORDS porcine circovirus type 2.

SOURCE porcine circovirus type 2

ORGANISM Viruses; ssDNA viruses; Circoviridae; Circovirus.

REFERENCE 1 (bases 1 to 1768)

AUTHORS Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A.,

Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.

Characterisation of PCV-2 isolates from Spain, Germany and France

Virus Res. 66 (1), 65-77 (2000)

20120936

10653918

2 (bases 1 to 1768)

Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A.,

Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.

Direct Submission

Submitted (03-NOV-1999) P24, Robert Koch Institut, Nordufer 20,

Berlin 13353, Germany

FEATURES

source

1..1768

/organism="porcine circovirus type 2"

/isolate="SPA2"

/db\_xref="taxon:85708"

/country="Spain"

complement(37..738)

/gene="cap"

complement(37..738)

/gene="cap"

/note="Cap"

/codon\_start=1

/product="putative capsid protein"

/protein\_id="AAF35301.1"

/db\_xref="GI:7021357"

/translation="MTYPRRRRRRRRSHLQILRRRPWLVHPRHRYRWRKNGI

FNRLSRTEGYTVKATTVRTPSWAVDMRFNIDDFVPPGGTNKISIPFEYYRIRKVK

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822..1766

/gene="rep"

822..1766

/gene="rep"

/note="Rep"

/codon\_start=1

/product="replicase"

/protein\_id="AAF35300.1"

/db\_xref="GI:7021356"

/translation="MPSKKNRSGPQPHKRWVFTLNNPSEDERKKIRELPISLFDYFI

VGEEGNEEGRTPHLQGFANFVKQTFNKVKWYLGARCHIEKAKGTDQONKEYCSKEGN

LLIECGAPRSQGSDLSTAVSTLLESGSLVTVAEQHPVTVFRNFRGLAELLKVSQGM

QKRDWKTNVHVIIVGPPGCGKSKWAFADPETTYWKPNKWDGYHGEVVVIDDFY

GWLPWDLLRLCDRYPLTVETKGTVPFLARSILITSNQTPLEWYSTAVPAVEALYR

RITSLVFWKNATEQSTEGGQFVTLSPPCPEFPYEINY"

BASE COUNT

456 a

358 c

500 g

454 t

ORIGIN

Query Match

89.3%; Score 626.8; DB 14; Length 1768;

Best Local Similarity

93.3%; Pred. No. 6.8e-169;

Matches 655; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY

1

ATGACGTATCCAAAGGAGCGTTACCGAAGAAGACACCGCCCGCAGCCATCTTGGC

60

Db

738

ATGACGTATCCAAAGGAGCGTTTCCGCAGACGACACCGCCCGCAGCCATCTTGGC

679

QY

61

CAGATCCTCCGCCCGCCCTCGGCTCGTCCACCCCGCCACCGTTACCGCTGGAGAAGG

120

Db

678

CAGATCCTCCGCCCGCCCTCGGCTCGTCCACCCCGCCACCGTTACCGCTGGAGAAGG

619

QY

121

AAAAATGGCATCTTCAACACCCCGCCTCTCCCGCACCTTCGGATATACTGTCAAGCGAACC

180

Db

618

AAAAATGGCATCTTCAACACCCCGCCTCTCCCGCACCTTCGGATATACTGTCAAGGCTACC

559

QY

181

ACAGTCAGAACGCCCTCCTGGCGGTGGACATGATGAGATTCAATATTAATGACTTTCTT

240

Db

558

ACAGTCAGAACGCCCTCCTGGCGGTGGACATGATGAGATTAAATATTAACGACTTTGTT

499

QY

241

CCCCCAGGAGGGGTCAAACCCCGCTCTGTGCCCTTTGAATACTACAGAATAAGAAAG

300

Db

498

CCCCCGGAGGGGGACCAACAAATCTCTATACCCCTTTGAATACTACAGAATAAGAAAG

439

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.

Characterisation of PCV-2 isolates from Spain, Germany and France

Virus Res. 66 (1), 65-77 (2000)

20120936

10653918

2 (bases 1 to 1768)

Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A.,

Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.

Direct Submission

Submitted (03-NOV-1999) P24, Robert Koch Institut, Nordufer 20,

Berlin 13353, Germany

FEATURES

Location/Qualifiers

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/organism="porcine circovirus type 2"

/isolate="SPA2"

/db\_xref="taxon:85708"

/country="Spain"

complement(37..738)

/gene="cap"

complement(37..738)

/gene="cap"

/note="Cap"

/codon\_start=1

/product="putative capsid protein"

/protein\_id="AAF35301.1"

/db\_xref="GI:7021357"

/translation="MTYPRRRRRRRRSHLQILRRRPWLVHPRHRYRWRKNGI

FNRLSRTEGYTVKATTVRTPSWAVDMRFNIDDFVPPGGTNKISIPFEYYRIRKVK

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822..1766

/gene="rep"

822..1766

/gene="rep"

/note="Rep"

/codon\_start=1

/product="replicase"

/protein\_id="AAF35300.1"

/db\_xref="GI:7021356"

/translation="MPSKKNRSGPQPHKRWVFTLNNPSEDERKKIRELPISLFDYFI

VGEEGNEEGRTPHLQGFANFVKQTFNKVKWYLGARCHIEKAKGTDQONKEYCSKEGN

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QKRDWKTNVHVIIVGPPGCGKSKWAFADPETTYWKPNKWDGYHGEVVVIDDFY

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BASE COUNT

456 a

358 c

500 g

454 t

ORIGIN

Query Match

89.3%; Score 626.8; DB 14; Length 1768;

Best Local Similarity

93.3%; Pred. No. 6.8e-169;

Matches 655; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY

1

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60

Db

738

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679

QY

61

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120

Db

678

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QY

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QY

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240

Db

558

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499

QY

241

CCCCCAGGAGGGGTCAAACCCCGCTCTGTGCCCTTTGAATACTACAGAATAAGAAAG

300

Db

498

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439



QY 301 GTTAAGTTGAATTCTGGCCCTGCTCCCGCATCACCCAGGGTGACAGGGGAGTGGGCTCC 360  
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Db 438 GTTAAGTTGAATTCTGGCCCTGCTCCCAATCACCCAGGGTGATAGGGGAGTGGGCTCC 379  
  
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Db 378 ACTGCTGTTATTTAGATGATAAATTTGTAAACAAGGCCACAGCCCTAACCTATGACCCC 319  
  
QY 421 TATGTAAACTACTTCCTCCGCCATACCATAACCCAGCCCTTCTCCTACCACCTCCCGGTAC 480  
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QY 481 TTTACCCCCAAACCTGTCCTAGATTTTCACTATTGATTACTTCCAACCAACAACAAGA 540  
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Db 258 TTTACCCCCAAACCTGTTCTTGATTCCACTATTGATTACTTCCAACCAATAACAAGAAG 199  
  
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Db 198 AATCAGCTTTGGCTGAGGCTACAAACCTCTGCAATGTGGACCACGTTAGGCCTCGGCACT 139  
  
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Db 78 TTCAGAGAAATTAATCTTAAAGACCCCCCACTTAAACCCTTAA 37

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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
CDS  
CDS  
CDS

AF086835 1768 bp DNA circular VRL 29-SEP-1998  
Porcine circovirus strain 9741, complete genome.  
AF086835  
AF086835.1 GI:3661518  
porcine circovirus.  
porcine circovirus  
Viruses; ssDNA viruses; Circoviridae; Circovirus.  
1 (bases 1 to 1768)  
Wang,L., Willison,P., Chow,B., Gibbons,E. and Babiuk,L.  
Emergence of a new porcine circovirus  
Unpublished  
2 (bases 1 to 1768)  
Wang,L., Willison,P., Chow,B., Gibbons,E. and Babiuk,L.  
Direct Submission  
Submitted (26-AUG-1998) VIDO, University of Saskatchewan, 120  
Veterinary Road, Saskatoon, Saskatchewan S7N 5E3, Canada  
Location/Qualifiers  
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Query Match 88.8%; Score 623.6; DB 14; Length 1768;  
Best Local Similarity 93.0%; Pred. No. 5.6e-168;  
Matches 653; Conservative 0; Mismatches 49; Indels 0; Gaps 0;  
  
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Db 1735 ATGACGTATCCAAGGAGGCGTTACCGCAGAAGAAGACACCGCCCCCGCAGCATCTTGGC 1676  
  
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Db 1675 CAGATCCTCCGCGCGCCCTGGCTCGTCCACCCCGCCACCGTTACCGCTGGAGAAG 1616  
  
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Db 1615 AAAAATGGCATCTTCAACACCCCGCCTCTCCGCGACCTTCGGATATACTGTCAAGCGTAAC 1556  
  
QY 181 ACAGTCAGAACGCCCTCCTGGCGGTGGACATGATGAGATTCAATATTAACTTCTT 240  
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Db 1555 ACAGTCAGAACGCCCTCCTGGCGGTGGACATGATGAGATTCAATATTAACTTCTT 1496  
  
QY 241 CCCCCAGGAGGGGGTCAAAACCCCGCTCTGTGCCCTTTTGAATACTACAGAATAAGAAAG 300  
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Db 1495 CCCCCAGGAGGGGGTCAAAACCCCGCTCTGTGCCCTTTTGAATACTACAGAATAAGAAAG 1436  
  
QY 301 GTTAAGTTGAATTTCTGGCCCTGCTCCCGCATACCCAGGGTGACAGGGGAGTGGGCTCC 360  
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Db 1435 GTTAAGTTGAATTTCTGGCCCTGCTCCCGCATACCCAGGGTGATAGGGGAGTGGGCTCC 1376  
  
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Db 1315 TATGTAAACTACTCTCCCGCCATACAATCCCCAACCCCTTCTCCTACCACCTCCCGGTAC 1256  
  
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Db 1135 GCGTTCGAAACAGTAAATACGACCAGGACTACAATATCCGTGTAAACCATGTATGACAA 1076  
  
QY 661 TTCAGAGAAATTAATTTTAAAGACCCCCCACTTAAACCCTTAA 702  
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RESULT 11  
AF109398/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
AF109398 1768 bp DNA circular VRL 23-JUL-2001  
Porcine circovirus type 2-C, complete genome.  
AF109398  
AF109398.1 GI:4106885  
porcine circovirus type 2-C.  
porcine circovirus type 2-C  
Viruses; ssDNA viruses; Circoviridae; Circovirus.  
1 (bases 1 to 1768)  
Hamel,A.L., Lin,L.L., Sachvie,C., Grudeski,E. and Nayar,G.P.  
PCR detection and characterization of type-2 porcine circovirus  
Can. J. Vet. Res. 64 (1), 44-52 (2000)  
20142849  
10680656



REFERENCE 2 (bases 1 to 1768)  
AUTHORS Hamel,A.L. and Nayar,G.P.S.  
TITLE Nucleotide sequence of four different isolates of circovirus detected in pigs with various clinical syndromes  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 1768)  
AUTHORS Hamel,A.L. and Nayar,G.P.S.  
TITLE Direct Submission  
JOURNAL Submitted (27-NOV-1998) Virology Laboratory, Veterinary Diagnostic Laboratory, Manitoba Agriculture, 545 University Crescent, Winnipeg, Manitoba R3T 5S6, Canada  
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source  
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/db\_xref="taxon:85543"  
/note="sequence obtained from several overlapping PCRs using DNA extracted from lung, mesenteric lymph node and tonsil of pig; similar to Porcine circovirus sequence presented in GenBank Accession Number AF027217; type-C designation is based upon restriction endonuclease digestion pattern"  
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51. .995  
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Query Match 88.8%; Score 623.6; DB 14; Length 1768;  
Best Local Similarity 93.0%; Pred. No. 5.6e-168;  
Matches 653; Conservative 0; Mismatches 49; Indels 0; Gaps 0;  
QY 1 ATGACGTATCCAAGGAGCGGTTACCGAAGAAGAAGACACCGCCCCCGCAGCCATCTTGGC 60  
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Db 1735 ATGACGTATCCAAGGAGCGGTTACCGCAGAAAGAGACCCGCCCGCAGCCATCTTGGC 1676  
QY 61 CAGATCCTCCGCCGCCCTCGTGGCTCGTCCACCCCGCCACCGTTACCGTGGAGAAGG 120  
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Db 1675 CAGATCCTCCGCCGCCCTCGTGGCTCGTCCACCCCGCCACCGTTACCGTGGAGAAGG 1616  
QY 121 AAAAATGGCATCTTCAACACCCCGCCTCTCCCGCACCTTCGGATATACTGTCAAGCGAACC 180  
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Db 1615 AAAAATGGCATCTTCAACACCCCGCCTCTCCCGCACCTTCGGATATACTGTCAAGGCTACC 1556  
QY 181 ACAGTCAGAACGCCCTCTCTGGCGGTGGACATGATGAGATTCAATATTAATGACTTTCTT 240  
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Db 1555 ACAGTCAGAACGCCCTCTCTGGCGGTGGACATGCTGAGATTTAAAATTGACGACTTTGTT 1496  
QY 241 CCCCCAGGAGGGGGTCAAAACCCCGCTCTGTGCCCTTTGAATACTACAGAATAAGAAAG 300  
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Db 1375 AGTGCTGTATTCTAGATGATAACTTTGTACCAAGGCCACAGCCCTAACCTATGACCCC 1316  
QY 421 TATGTAACTACTCTCCCGCCATACCAATAACCCAGCCCTTCTCCTACCACCTCCCGGTAC 480  
|||||

Db	1315	TATGTAAACTACTCTCCCGCCATACCATAACCCAGCCCTTCTCCTACCACCTCCCGTTAA	1256
QY	481	TTTACCCCCAACCTGTCTCTAGATTTCACTATTGATTACTTCCAAACCAACAACAAAGA	540
Db	1255	TTACACCCCAACCTGTCTTGATGGGACAATCGATTACTTCCAAACCCCAATAACAAGA	1196
QY	541	AACCAGCTGTGGCTGAGACTACAAACTGCTGGAATGTAGACCACGTTAGGCCTCGGCACT	600
Db	1195	AATCAACTCTGGCTGAGACTACAAACTACTGGAATGTAGACCATGTAGGCCTCGGCACT	1136
QY	601	GCJTTCGAAACAGTATATACGACCAGGAATACATATATCCGTGTAAACCATGTATGTACAA	660
Db	1135	CGTTCGAAACAGTATATACGACCAGGACTACATATATCCGTGTAAACCATGTATGTACAA	1076
QY	661	TTCAGAGAAATTAATTTAAAGACCCCCACCTTAACCCCTTAA	702
Db	1075	TTCAGAGAAATTAATCTTAAGACCCCCACCTTAACCCCTTAA	1034
RESULT 12			
AF154679/c		1768 bp	DNA
LOCUS	AF154679	Porcine circovirus, complete genome.	circular VRL 13-JUN-1999
DEFINITION	AF154679	Porcine circovirus, complete genome.	
ACCESSION	AF154679		
VERSION	AF154679.1	GI:5052004	
KEYWORDS		porcine circovirus.	
SOURCE		porcine circovirus	
ORGANISM		Viruses; ssDNA viruses; Circoviridae; Circovirus.	
REFERENCE		1 (bases 1 to 1768)	
AUTHORS		Kuo,T.Y., Chiou,Y.C. and Lai,S.S.	
TITLE		Complete nucleotide sequences analysis of porcine circovirus outbreak in Taiwan	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 1768)	
AUTHORS		Kuo,T.Y., Chiou,Y.C. and Lai,S.S.	
TITLE		Direct Submission	
JOURNAL		Submitted (27-MAY-1999) Veterinary Medicine, National Taiwan University, 142, Chousan Road, Taipei 106, Taiwan	
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source		Location/Qualifiers	
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ORIGIN		455 t	
Query Match 88.8%; Score 623.6; DB 14; Length 1768;			
Best Local Similarity 93.0%; Pred. No. 5.6e-168;			
Matches 653; Conservative 0; Mismatches 49; Indels 0; Gaps 0;			
QY	1	ATGACGTATCCAAGAGCGGTTACCGAAGAAGAACACCGCCCCCGCAGCCATCTTGGC	60
Db	1735	ATGACGTATCCAAGAGCGGTTTCCGCAGACGACACCGCCCCCGCAGCCATCTTGGC	1676
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Db	1675	CAATCCTCCGCGCGCCCTCGTCTCCACCCCGCCACCGTTACCGCTGGAGAAGG	1616
QY	121	AAAAATGGCATCTTCAACACCCCGCCTCTCCCGCACCTTCGGATATACTGTCAACGGAACC	180

Db	1615	AAAAATGGCATCTTCAACACCCCGCCTCTCCGCACCTTCGGATATACTGTCAAGGCTAGC	1556
QY	181	ACAGTCAGAACGCCCTCCTGGCGGTGGACATGATGAGATTCAATATTAATGACTTTCTT	240
Db	1555	ACAGTCAGAACGCCCTCCTGGCGGTGGACATGATGAGATTGATATTAACGACTTTGTT	1496
QY	241	CCCCCAGGAGGGGTCAAAACCCCGCTCTGTGCCCTTTGAATACTACAGAATAAGAAAG	300
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QY	301	GTTAAGTTGAATTTGGCCCTGCTCCCGCATCACCCAGGGTGACAGGGAGTGGGCTCC	360
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QY	361	AGTGCTGTATTTTAGATGATAACTTTGTAAACAAAGGCCACAGCCCTCACCTATGACCCC	420
Db	1375	ACTGCTGTATTTTAGATGATAACTTTGTAACTAAGGCCACAGCCCTAACCTATGACCCC	1316
QY	421	TATGTAAACTACTCTCCCGCCATACCATAACCCAGCCCTTCTCCTACCACCTCCCGGTAC	480
Db	1315	TATGTAAACTACTCTCCCGCCATACAATCCCCAACCCCTTCTCCTACCACCTCCCGGTAC	1256
QY	481	TTTACCCCAAAACCTGTCTAGATTTCACTATTGATTACTTCCAAACCAACAACAAAGA	540
Db	1255	TTTACCCCAAAACCTGTCTTGAATTCCTACTATTGATTACTTCCAAACCAACAACAAAGG	1196
QY	541	AACCAAGCTGTGGTGAGACTACAAACTGCTGGAATGTAGACCACGTAGGCTCGGCACT	600
Db	1195	AATCAGCTTGGCTGAGGCTACAAACCTCGCAAAATGTGGACCACGTAGGCTCGGCACT	1136
QY	601	CGTTCGAAACAGTATATACGACCAGGAATACAATATCCGTGTAAACCATGTATGTACAA	660
Db	1135	CGTTCGAAACAGTAAATACACCAGGACTACAATATCCGTGTAAACCATGTATGTACAA	1076
QY	661	TTCAGAGAAATTAATTTTAAAGACCCCCCCTTAACCCCTTAA	702
Db	1075	TTCAGAGAAATTAATCTTAAAGACCCCCCCTTAACCCCTTAA	1034
RESULT 13			
AF166528/c		1768 bp	mRNA
LOCUS	AF166528	Porcine circovirus complete genome.	linear VRL 19-AUG-1999
DEFINITION	AF166528	Porcine circovirus complete genome.	
ACCESSION	AF166528		
VERSION	AF166528.1	GI:5739338	
KEYWORDS		porcine circovirus.	
SOURCE		porcine circovirus	
ORGANISM		Viruses; ssDNA viruses; Circoviridae; Circovirus.	
REFERENCE		1 (bases 1 to 1768)	
AUTHORS		Yang,K.H., Lee,Y.F., Chao,D.S., Shieh,Y.C. and Lai,S.S.	
TITLE		Complete nucleotide sequences of porcine circovirus Tainan strand outbreak in Taiwan	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 1768)	
AUTHORS		Yang,K.H., Lee,Y.F., Chao,D.S., Shieh,Y.C. and Lai,S.S.	
TITLE		Direct Submission	
JOURNAL		Submitted (08-JUL-1999) Veterinary Medicine, National Chia-yi Institute of Technology, 300 Shei Fu Road, Lu Liao Li, Chia-Yi City 600, Taiwan	
FEATURES			
source		Location/Qualifiers	
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CDS			

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ORIGIN

Query Match 88.8%; Score 623.6; DB 14; Length 1768;  
Best Local Similarity 93.0%; Pred. No. 5.6e-168;  
Matches 653; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

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Db 1675 CAGATCCTCCGCCCGCCCTCGGCTCGTCCACCCCGCCACCGTTACCGCTGGAGAAG 1616  
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QY 121 AAAAATGGCATCTTCAACACCCGCTCTCCCGCACCTTCGGATATACTGTCAAGCGAAC 180  
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QY 181 ACAGTCAGAACGCCCTCCTGGGCGGTGGACATGATGAGATTCAATATTAATGACTTTCTT 240  
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QY 241 CCCCCAGGAGGGGGTCAACCCCGCTCTGTGCCCTTTGATATACTACAGAATAAGAAAG 300  
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QY 301 GTTAAGGTTGAATTCTGGCCCTGCTCCCGCATCACCCAGGTTACAGGGGAGTGGGCTCC 360  
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Db 1435 GTTAAGGTTGAATTCTGGCCCTGTTCCCAATCACCCAGGTTACAGGGGAGTGGGCTCC 1376  
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QY 361 AGTGCTGTTATTTTAGATGATAAATTTGTAACAAAGGCCACAGCCCTCACCTATGACCCC 420  
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Db 1375 ACTGCTGTTATTTCTAGATGATAAATTTGTAACTAAGGCCACAGCCCTAACCTATGACCCG 1316  
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QY 541 AACCAGCTGTGGCTGAGACTACAAACTGCTGGAAATGTAGACCACGTAGGCCTCGGCAC 600  
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QY 661 TTCAGAGAATTTAATTTTAAAGACCCCCCACTTAACCCCTAA 702  
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RESULT 14  
AF201307/c 1768 bp DNA circular VRL 23-FEB-2000  
LOCUS  
DEFINITION Porcine circovirus type 2 isolate GER3, complete genome.  
ACCESSION AF201307  
VERSION AF201307.1 GI:7021349  
KEYWORDS  
SOURCE porcine circovirus type 2.  
ORGANISM porcine circovirus type 2  
Viruses; ssDNA viruses; Circoviridae; Circovirus.  
REFERENCE 1 (bases 1 to 1768)

AUTHORS Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A., Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.  
TITLE Characterisation of PCV-2 isolates from Spain, Germany and France  
JOURNAL Virus Res. 66 (1), 65-77 (2000)  
MEDLINE 20120936  
PUBMED 10653918  
REFERENCE 2 (bases 1 to 1768)  
AUTHORS Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A., Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.  
TITLE Direct Submission  
JOURNAL Submitted (03-NOV-1999) P24, Robert Koch Institut, Nordufer 20, Berlin 13353, Germany

FEATURES  
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BASE COUNT 446 a 357 c 503 g 462 t  
ORIGIN  
Query Match 88.8%; Score 623.6; DB 14; Length 1768;  
Best Local Similarity 93.0%; Pred. No. 5.6e-168;  
Matches 653; Conservative 0; Mismatches 49; Indels 0; Gaps 0;  
QY 1 ATGACGTATCCAAGGAGGCGGTACCGAAGAAGACACCCGCCCGCAGCCATCTTGGC 60  
|||||  
Db 738 ATGACGTATCCAAGGAGGCGGTTCGCGACGACGACACCGCGCCGAGCCATCTTGGC 679  
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QY 61 CAGATCCTCCGCCCGCCCTCGGCTCGTCCACCCCGCCACCGTTACCGCTGGAGAAG 120  
|||||  
Db 678 CAGATCCTCCGCCCGCCCTCGGCTCGTCCACCCCGCCACCGTTACCGCTGGAGAAG 619  
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QY 121 AAAAATGGCATCTTCAACACCCCGCTCTCCCGCACCTTCGGATATACTGTCAAGCGAAC 180  
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Db 618 AAAAATGGCATCTTCAACACCCCGCTCTCCCGCACCTTCGGATATACTGTCAAGGCTACC 559  
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QY 181 ACAGTCAGAACGCCCTCCTGGGCGGTGGACATGATGAGATTCAATATTAATGACTTTCTT 240  
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Db 558 ACAGTCACAACGCCCTCCTGGGCGGTGGACATGATGAGATTTAATATTAACGACTTTGTT 499  
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Db 498 CCCCCGAGGGGGGACCAACAAATCTCTATACCCCTTTGAATATACTACAGAATAAGAAAG 439  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2003, 09:15:38 ; Search time 2022 Seconds  
(without alignments)  
10103.941 Million cell updates/sec

Title: US-09-514-245B-25  
Perfect score: 702  
Sequence: 1 atgacgtatccaaggaggcg.....acccccacttaacccttaa 702

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_htg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vi: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
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32: em\_htg\_other: \*  
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34: em\_htg\_pln: \*  
35: em\_htg\_rod: \*  
36: em\_htg\_mam: \*  
37: em\_htg\_vrt: \*  
38: em\_sy: \*  
39: em\_htgo\_hum: \*  
40: em\_htgo\_mus: \*  
41: em\_htgo\_other: \*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	702	100.0	702	6	AX003277	AX003277 Sequence
C 2	702	100.0	1767	6	AX003274	AX003274 Sequence
3	702	100.0	1767	6	AX003275	AX003275 Sequence
C 4	698.8	99.5	1767	14	AF201311	AF201311 Porcine C
C 5	698.8	99.5	1767	14	AY122275	AY122275 Porcine C
C 6	690.8	98.4	1767	14	AF201897	AF201897 Porcine C
C 7	682.8	97.3	1766	14	PCI293869	AJ293869 Porcine C
C 8	643.4	91.7	1767	14	AY035820	AY035820 Porcine C
C 9	626.8	89.3	1768	14	AF201309	AF201309 Porcine C
C 10	623.6	88.8	1768	14	AF086835	AF086835 Porcine C
C 11	623.6	88.8	1768	14	AF109398	AF109398 Porcine C
C 12	623.6	88.8	1768	14	AF154679	AF154679 Porcine C
C 13	623.6	88.8	1768	14	AF166528	AF166528 Porcine C
C 14	623.6	88.8	1768	14	AF201307	AF201307 Porcine C
C 15	623.6	88.8	1768	14	AF465211	AF465211 Porcine C
C 16	622	88.6	1768	14	AB072302	AB072302 Porcine C
C 17	622	88.6	1768	14	AF201308	AF201308 Porcine C
C 18	622	88.6	1768	14	AF201310	AF201310 Porcine C
C 19	622	88.6	2520	6	AX068058	AX068058 Sequence
C 20	622	88.6	3609	6	AX068062	AX068062 Sequence
C 21	620.4	88.4	1768	14	AF027217	AF027217 Porcine C
C 22	620.4	88.4	1768	14	AF085695	AF085695 Porcine C
C 23	620.4	88.4	1768	14	AF086836	AF086836 Porcine C
C 24	618.8	88.1	1768	14	AF086834	AF086834 Porcine C
C 25	618.8	88.1	1768	14	AF118095	AF118095 Porcine C
C 26	618.8	88.1	1768	14	AF264042	AF264042 Porcine C
C 27	618.8	88.1	1768	14	AF381175	AF381175 Porcine C
C 28	618.8	88.1	1768	14	AF381177	AF381177 Porcine C
C 29	617.2	87.9	1768	6	AX092147	AX092147 Sequence
C 30	617.2	87.9	1768	14	AB072303	AB072303 Porcine C
C 31	617.2	87.9	1768	14	PCAJ3185	AJ223185 Porcine C
C 32	615.6	87.7	1768	14	AB072301	AB072301 Porcine C
C 33	615.6	87.7	1768	14	AF112862	AF112862 Porcine C
C 34	615.6	87.7	1768	14	AF264039	AF264039 Porcine C
C 35	615.6	87.7	1768	14	AF264040	AF264040 Porcine C
C 36	614	87.5	1768	6	AX379561	AX379561 Sequence
C 37	614	87.5	1768	6	AX379562	AX379562 Sequence
C 38	614	87.5	1768	6	AX379563	AX379563 Sequence
C 39	614	87.5	1768	14	AF109397	AF109397 Bovine cl
C 40	614	87.5	1768	14	AF118097	AF118097 Porcine C
C 41	614	87.5	1768	14	AF381176	AF381176 Porcine C
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C 43	614	87.5	1768	14	AY099495	AY099495 Porcine C
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ALIGNMENTS

RESULT 1  
AX003277  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

AX003277  
Sequence 12 from Patent WO9929871.  
AX003277  
AX003277.1 GI:9927101

702 bp

DNA

linear

PAT 24-AUG-2000

porcine circovirus.  
porcine circovirus  
Viruses; ssDNA viruses; Circoviridae; Circovirus.  
1 (bases 1 to 702)  
Hutet,E. and Albina,E.  
Circovirus sequences related to piglet weight loss disease (pwd)  
Patent: WO 9929871-A 12 17-JUN-1999;  
HUTET EVELYNE (FR); ALBINA EMMANUEL (FR)

[illegible]

KW porcine multisystemic wasting syndrome; pig; vaccine; ss.

XX Porcine circovirus.

OS FR2769322-A1.

XX 09-APR-1999.

XX 22-JAN-1998; 98FR-0000873.

PF 03-OCT-1997; 97FR-0012382.

XX (MERI-) MERIAL SAS.

XX Allan G, Chappuis GE, Charreyre CE, Clark E, Ellis J;

PI Haines D, Harding J, Hassard L, Meehan B;

XX WPI; 1999-246948/21.

XX New type II porcine circovirus, used for, e.g. passive immunization

PT of pregnant sows

XX Claim 14; Fig 2; 48pp; French.

XX The present sequence represents the nucleotide sequence of PCV isolate  
CC Impl011-48285. The specification describes a preparation of type II  
CC porcine circovirus (PCV), which is particularly isolated from a lesion,  
CC from a pig with symptoms of PMWS (porcine multisystemic wasting  
CC syndrome). PCV (attenuated or inactivated), polypeptides derived from  
CC it, and vectors that express these polypeptides are all useful in  
CC vaccines, suitable for administration to adult or young pigs, or to  
CC pregnant sows (for passive immunization of their offspring). DNA  
CC isolated from PCV is used for in vivo or in vitro expression of viral  
CC polypeptides, also as probes or primers for diagnosis in usual  
CC hybridization or amplification assays. These polypeptides may also be  
CC used diagnostically to detect PCV-specific antibodies, while antibodies  
CC raised against the polypeptides can be used to detect antigens, in any  
CC usual immunoassay format.

XX SQ Sequence 1767 BP; 448 A; 359 C; 500 G; 460 T; 0 other;

Query Match 53.9%; Score 378.4; DB 20; Length 1767;  
Best Local Similarity 98.5%; Pred. No. 5.2e-104;  
Matches 382; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 375 AGATGATAACTTTGTAAACAAAGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTC 434  
Db |||||  
1707 AGATGATAACTTTGTAAACAAAGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTC 1648

QY 435 CTCCCGCCATACCATACCCAGCCCTTCTCTACCACTCCCGGTACTTTACCCCAAAACC 494  
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Db |||||  
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Db |||||  
1467 TATATACGACCAGGAATACAATATCCGTGTAAACCATGTATGTACAATTCAGAGAATTAA 1408

QY 675 TTTTAAAGACCCCTTAAACCCCTTAA 702

Db |||||  
1407 TCTTAAAGACCCCTTAAACCCCTTAA 1380



Best Local Similarity 99.0%; Pred. No. 5.6e-105;  
Matches 384; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 375 AGATGATAAAGTTTGTAAAGGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTC 434  
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Db 1707 AGATGATAAAGTTTGTAAAGGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTC 1648

QY 435 CTCCCGCCATACCATACCCAGCCCTTCTCCTACCACTCCCGGTACTTTACCCCAAACC 494  
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Db 1647 CTCCCGCCATACCATACCCAGCCCTTCTCCTACCACTCCCGGTACTTTACCCCAAACC 1588

QY 495 TGTCTAGATTTCACATATTGATTACTTCCAACCAACAACAAGAAACCAAGCAAGCTGTGGCT 554  
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RESULT 12  
AAZ56869/c  
ID AAZ56869 standard; DNA; 1767 BP.

XX AC AAZ56869;

XX DT 25-APR-2000 (first entry)

DE DNA sequence of PCV Imp.1011-48121 isolate.

XX KW Antigen; porcine multisystemic wasting syndrome; PMWS; antiviral;  
KW porcine circovirus; PCV; porcine parvovirus; PPV; vaccination; ds.

XX OS Porcine circovirus.

XX PN WO200001409-A2.

PD 13-JAN-2000.

XX PF 28-JUN-1999; 99WO-EP04698.

XX PR 06-JUL-1998; 98FR-0008777.

XX PA (MERI-) MERIAL.  
PA (UYBE-) UNIV QUEENS BELFAST.  
PA (UYSA-) UNIV SASKATCHEWAN.

XX PI Allan GM, Meehan BM, Ellis JA, Krakowka GS, Audonnet JF;  
XX WPI: 2000-182091/16.

XX PT Use of a porcine circovirus antigen and a porcine parvovirus antigen  
PT for vaccination against porcine multisystemic wasting syndrome -

XX PS Disclosure; Fig 1; 61pp; English.

XX CC The invention provides a novel antigenic preparation directed against  
CC porcine multisystemic wasting syndrome (PMWS) that comprises porcine  
CC circovirus (PCV) antigen and porcine parvovirus (PPV) antigen. The PCV  
CC antigens and PPV antigens can be used for vaccination against PMWS. The  
CC present sequence represents the DNA sequence of PCV Imp.1011-48121

CC isolate.  
XX SQ Sequence 1767 BP; 447 A; 360 C; 502 G; 458 T; 0 other;

Query Match 54.4%; Score 381.6; DB 21; Length 1767;  
Best Local Similarity 99.0%; Pred. No. 5.6e-105;  
Matches 384; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 315 CTGGCCCTGCTCCCGCATCACCCAGGGTGACAGGGAGTGGGCTCCAGTGCCTGTTATTTT 374  
|||||  
Db 1767 CTGGCCCTGCTCCCGCATCACCCAGGGTGACAGGGAGTGGGCTCCAGTGCCTGTTATTTCT 1708

QY 375 AGATGATAAAGTTTGTAAAGGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTC 434  
|||||  
Db 1707 AGATGATAAAGTTTGTAAAGGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTC 1648

QY 435 CTCCCGCCATACCATACCCAGCCCTTCTCCTACCACTCCCGGTACTTTACCCCAAACC 494  
|||||  
Db 1647 CTCCCGCCATACCATACCCAGCCCTTCTCCTACCACTCCCGGTACTTTACCCCAAACC 1588

QY 495 TGTCTAGATTTCACATATTGATTACTTCCAACCAACAACAAGAAACCAAGCAAGCTGTGGCT 554  
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Db 1587 TGTCTAGATTTCACATATTGATTACTTCCAACCAACAACAAGAAACCAAGCAAGCTGTGGCT 1528

QY 555 GAGACTACAAACTGCTGGAATGTAGACCACGTAGGCCTCGGCACCTGCGTTTCGAAACAG 614  
|||||  
Db 1527 GAGACTACAAACTGCTGGAATGTAGACCACGTAGGCCTCGGCACCTGCGTTTCGAAACAG 1468

QY 615 TATATACGACCGAATACAAATATCCGTGTAAACCATGTATGTACAATTTCAGAGAAATTAA 674  
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Db 1467 TATATACGACCGAATACAAATATCCGTGTAAACCATGTATGTACAATTTCAGAGAAATTAA 1408

QY 675 TTTTAAAGACCCCACTTAACCCTTAA 702  
|  
Db 1407 TCTTAAAGACCCCACTTAACCCTTAA 1380

RESULT 13  
AAZ56835/c  
ID AAF75835 standard; DNA; 1767 BP.

XX AC AAF75835;

XX DT 18-MAY-2001 (first entry)

DE PCV DNA fragment of Imp 1011-48121 strain.

XX KW Vaccine; pig; myocarditis; abortion; intrauterine infection;  
KW multisystemic wasting syndrome; ds.

XX OS Porcine circovirus-2.

XX PN WO200116330-A2.

XX PD 08-MAR-2001.

XX PF 28-AUG-2000; 2000WO-EP08781.

XX PR 31-AUG-1999; 99US-0151564.  
PR 31-MAY-2000; 2000US-0583350.

XX PA (MERI-) MERIAL.  
PA (UYSA-) UNIV SASKATCHEWAN.  
PA (UYBE-) UNIV QUEENS BELFAST.

XX PI Ellis JA, Allan GM, Meehan B, Clark E, Haines D, Hassard L;  
PI Harding J, Charreyre CE, Chappuis GE, Krakowka GS, Audonnet JF;  
PI Mcneilly F;

XX WPI: 2001-244408/25.

DR Use of porcine circovirus-2 immunogen to formulate a vaccine  
XX composition to treat pigs against myocarditis, abortion, intrauterine

PT infection and/or post-weaning, multisystemic wasting syndrome  
PT associated with PCV-2  
XX  
PS Disclosure; Fig.1 #2; 134pp; English.  
XX  
CC The present invention relates to the use of porcine circovirus-2 (PCV-2)  
CC immunogen to formulate a vaccine composition to prevent or treat pigs  
CC against myocarditis and/or abortion and/or intrauterine infection and/or  
CC post-weaning, multisystemic wasting syndrome and other pathological  
CC sequelae associated with PCV-2. The present sequence is a DNA fragment of  
CC a strain of PCV, which was used in the present invention.  
XX  
SQ Sequence 1767 BP; 447 A; 360 C; 502 G; 458 T; 0 other;

Query Match 54.4%; Score 381.6; DB 22; Length 1767;  
Best Local Similarity 99.0%; Pred. No. 5.6e-105;  
Matches 384; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 315 CTGGCCCTGCTCCCGATACCCAGGGTGACAGGGGAGTGGGCTCCAGTGTGTTATTT 374  
Db |||||||  
QY 1767 CTGGCCCTGCTCCCGATACCCAGGGTGACAGGGGAGTGGGCTCCAGTGTGTTATTT 1708  
Db |||||||  
QY 375 AGATGATAACTTTGTACAAAGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTC 434  
Db |||||||  
QY 1707 AGATGATAACTTTGTACAAAGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTC 1648  
Db |||||||  
QY 435 CTCCCGCCATACCATAACCCAGCCCTTCTCTACCACTCCCGGTACTTTACCCCCAAACC 494  
Db |||||||  
QY 1647 CTCCCGCCATACCATAACCCAGCCCTTCTCTACCACTCCCGGTACTTTACCCCCAAACC 1588  
Db |||||||  
QY 495 TGTCTTAGATTTCACCTATTGATTACTTCCAAACCAACAAAGAAACACAGCTGTGGCT 554  
Db |||||||  
QY 1587 TGTCTTAGATTTCACCTATTGATTACTTCCAAACCAACAAAGAAACACAGCTGTGGCT 1528  
Db |||||||  
QY 555 GAGACTACAAACTGCTGGAATGTAGACCACGCTAGGCCCTCGGCACCTGCGTTTCGAAACAG 614  
Db |||||||  
QY 1527 GAGACTACAAACTGCTGGAATGTAGACCACGCTAGGCCCTCGGCACCTGCGTTTCGAAACAG 1468  
Db |||||||  
QY 615 TATATACGACCAAGGATACAATATCCGTGTAAACCATGTATGTACAATTTCAGAGAAATTAA 674  
Db |||||||  
QY 1467 TATATACGACCAAGGATACAATATCCGTGTAAACCATGTATGTACAATTTCAGAGAAATTAA 1408  
Db |||||||  
QY 675 TTTTAAAGACCCCTTAACCCCTTAA 702  
Db |||||||  
QY 1407 TCTTAAAGACCCCTTAACCCCTTAA 1380  
Db |||||||

RESULT 14  
AAX35379/c  
ID AAX35379 standard; DNA; 1767 BP.  
XX  
AC AAX35379;  
XX  
DT 07-JUL-1999 (first entry)  
XX  
DE Nucleotide sequence of PCV isolate Impl011-48285.  
XX

KW PCV isolate; type II porcine circovirus; PCV; PMWS;  
KW porcine multisystemic wasting syndrome; pig; vaccine; ss.  
XX  
OS Porcine circovirus.

PN WO9918214-A1.  
XX  
PD 15-APR-1999.  
XX  
PF 01-OCT-1998; 98WO-FR02107.  
XX  
PR 20-MAR-1998; 98FR-0003707.  
PR 03-OCT-1997; 97FR-0012382.  
PR 22-JAN-1998; 98FR-0000873.  
XX  
PA (MERI-) MERIAL.

PA (UYBE-) UNIV QUEENS BELFAST.  
PA (UYSA-) UNIV SASKATCHEWAN.  
XX  
PI Allan G, Chappuis GE, Charreyre CE, Clark E, Ellis J;  
PI Haines D, Harding J, Hassard L, Meehan B;  
XX  
DR WPI; 1999-264024/22.  
XX  
PT New type II porcine circovirus  
XX  
PS Claim 11; Fig 2; 56pp; French.  
XX

CC The present sequence represents the nucleotide sequence of PCV isolate  
CC Impl011-48285. The specification describes a preparation of type II  
CC porcine circovirus (PCV), which is particularly isolated from a lesion,  
CC from a pig with symptoms of PMWS (porcine multisystemic wasting  
CC syndrome). PCV (attenuated or inactivated), polypeptides derived from  
CC it, and vectors that express these polypeptides are all useful in  
CC vaccines, suitable for administration to adult or young pigs, or to  
CC pregnant sows (for passive immunization of their offspring). DNA  
CC isolated from PCV is used for in vivo or in vitro expression of viral  
CC polypeptides, also as probes or primers for diagnosis in usual  
CC hybridization or amplification assays. These polypeptides may also be  
CC used diagnostically to detect PCV-specific antibodies, while antibodies  
CC raised against the polypeptides can be used to detect antigens, in any  
CC usual immunoassay format.  
XX

SQ Sequence 1767 BP; 448 A; 359 C; 500 G; 460 T; 0 other;

Query Match 53.9%; Score 378.4; DB 20; Length 1767;  
Best Local Similarity 98.5%; Pred. No. 5.2e-104;  
Matches 382; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 315 CTGGCCCTGCTCCCGATACCCAGGGTGACAGGGGAGTGGGCTCCAGTGTGTTATTT 374  
Db |||||||  
QY 1767 CTGGCCCTGCTCCCGATACCCAGGGTGACAGGGGAGTGGGCTCCAGTGTGTTATTT 1708  
Db |||||||  
QY 375 AGATGATAACTTTGTACAAAGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTC 434  
Db |||||||  
QY 1707 AGATGATAACTTTGTACAAAGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTC 1648  
Db |||||||  
QY 435 CTCCCGCCATACCATAACCCAGCCCTTCTCTACCACTCCCGGTACTTTACCCCCAAACC 494  
Db |||||||  
QY 1647 CTCCCGCCATACCATAACCCAGCCCTTCTCTACCACTCCCGGTACTTTACCCCCAAACC 1588  
Db |||||||  
QY 495 TGTCTTAGATTTCACCTATTGATTACTTCCAAACCAACAAAGAAACACAGCTGTGGCT 554  
Db |||||||  
QY 1587 TGTCTTAGATTTCACCTATTGATTACTTCCAAACCAACAAAGAAATCAGCTGTGGCT 1528  
Db |||||||  
QY 555 GAGACTACAAACTGCTGGAATGTAGACCACGCTAGGCCCTCGGCACCTGCGTTTCGAAACAG 614  
Db |||||||  
QY 1527 GAGACTACAAACTGCTGGAATGTAGACCACGCTAGGCCCTCGGCACCTGCGTTTCGAAACAG 1468  
Db |||||||  
QY 615 TATATACGACCAAGGATACAATATCCGTGTAAACCATGTATGTACAATTTCAGAGAAATTAA 674  
Db |||||||  
QY 1467 TATATACGACCAAGGATACAATATCCGTGTAAACCATGTATGTACAATTTCAGAGAAATTAA 1408  
Db |||||||  
QY 675 TTTTAAAGACCCCTTAACCCCTTAA 702  
Db |||||||  
QY 1407 TCTTAAAGACCCCTTAACCCCTTAA 1380  
Db |||||||

RESULT 15  
AAX35211/c  
ID AAX35211 standard; DNA; 1767 BP.  
XX  
AC AAX35211;  
XX  
DT 01-JUL-1999 (first entry)  
XX  
DE Nucleotide sequence of PCV isolate Impl011-48285.  
XX  
KW PCV isolate; type II porcine circovirus; PCV; PMWS;

QY 653 ATGTACAATTCAGAGAAATTAATTTTAAAGACCCCCCACTTAACCCCTTAA 702  
Db 664 ATGTACAATTCAGAGAAATTAATCTTAAAGACCCCCCACTTAACCCCTAA 615

RESULT 10

AAX35378/C  
ID AAX35378 standard; DNA; 1767 BP.  
XX  
AC AAX35378;  
XX  
DT 07-JUL-1999 (first entry)  
XX  
DE Nucleotide sequence of PCV isolate Impl011-48121.  
XX  
KW PCV isolate; type II porcine circovirus; PCV; PMWS;  
KW porcine multisystemic wasting syndrome; pig; vaccine; ss.  
XX  
OS Porcine circovirus.  
XX

PN WO9918214-A1.  
XX  
PD 15-APR-1999.  
XX  
PF 01-OCT-1998; 98WO-FR02107.  
XX  
PR 20-MAR-1998; 98FR-0003707.  
PR 03-OCT-1997; 97FR-0012382.  
PR 22-JAN-1998; 98FR-0000873.  
XX  
PA (MERI-) MERIAL.  
PA (UYBE-) UNIV QUEENS BELFAST.  
PA (UYSA-) UNIV SASKATCHEWAN.  
XX  
PI Allan G, Chappuis GE, Charreyre CE, Clark E, Ellis J;  
PI Haines D, Harding J, Hassard L, Meehan B;  
XX  
DR WPI; 1999-264024/22.  
XX  
PT New type II porcine circovirus  
XX  
PS Claim 11; Fig 1; 56pp; French.

CC The present sequence represents the nucleotide sequence of PCV isolate  
CC Impl011-48121. The specification describes a preparation of type II  
CC porcine circovirus (PCV), which is particularly isolated from a lesion,  
CC from a pig with symptoms of PMWS (porcine multisystemic wasting  
CC syndrome). PCV (attenuated or inactivated), polypeptides derived from  
CC it, and vectors that express these polypeptides are all useful in  
CC vaccines, suitable for administration to adult or young pigs, or to  
CC pregnant sows (for passive immunization of their offspring). DNA  
CC isolated from PCV is used for in vivo or in vitro expression of viral  
CC polypeptides, also as probes or primers for diagnosis in usual  
CC hybridization or amplification assays. These polypeptides may also be  
CC used diagnostically to detect PCV-specific antibodies, while antibodies  
CC raised against the polypeptides can be used to detect antigens, in any  
CC usual immunoassay format.

SQ Sequence 1767 BP; 447 A; 360 C; 502 G; 458 T; 0 other;

Query Match 54.4%; Score 381.6; DB 20; Length 1767;  
Best Local Similarity 99.0%; Pred. No. 5.6e-105;  
Matches 384; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 315 CTGGCCCTGCTCCCGATCACCCAGGGTGACAGGGGAGTGGGCTCCAGTGGTGTATTTT 374  
Db 1767 CTGGCCCTGCTCCCGATCACCCAGGGTGACAGGGGAGTGGGCTCCAGTGGTGTATTTCT 1708  
QY 375 AGATGATAACTTTGTACAAAGGCCACAGCCCTACCTATGACCCCTATGTAAACTACTC 434  
Db 1707 AGATGATAACTTTGTACAAAGGCCACAGCCCTACCTATGACCCCTATGTAAACTACTC 1648

QY 435 CTCCCGCCATACCAFAACCCAGCCCTTCTCCTACCACTCCCGGTACTTTACCCCCCAACCC 494

Db 1647 CTCCCGCCATACCAATAACCCAGCCCTTCTCCTACCACTCCCGTACTTTACCCCAACCC 1588  
QY 495 TGTCTAGATTTCACATATTGATTACTTCCAACCAACAAACAAAGAAACCAAGTGTGGCT 554  
Db 1587 TGTCTAGATTCCACTATTGATTACTTCCAACCAACAAACAAAGAAACCAAGTGTGGCT 1528  
QY 555 GAGACTACAAACTGCTGGAAATGTAGACCACTAGGCCTCGGCACGTGCGTTGCAAAACAG 614  
Db 1527 GAGACTACAAACTGCTGGAAATGTAGACCACTAGGCCTCGGCACGTGCGTTGCAAAACAG 1468  
QY 615 TATATACGACCAGGAATACAATATCCGTGTAACCATGTATGTACAATTCAGAGAATTTAA 674  
Db 1467 TATATACGACCAGGAATACAATATCCGTGTAACCATGTATGTACAATTCAGAGAATTTAA 1408  
QY 675 TTTTAAAGACCCCCCACTTAACCCTTAA 702  
Db 1407 TCTTAAAGACCCCCCACTTAACCCTTAA 1380

RESULT 11

AAX35210/C  
ID AAX35210 standard; DNA; 1767 BP.  
XX  
AC AAX35210;  
XX  
DT 01-JUL-1999 (first entry)  
XX  
DE Nucleotide sequence of PCV isolate Impl011-48121.  
XX  
KW PCV isolate; type II porcine circovirus; PCV; PMWS;  
KW porcine multisystemic wasting syndrome; pig; vaccine; ss.  
XX  
OS Porcine circovirus.  
XX  
PN FR2769322-A1.  
XX  
PD 09-APR-1999.  
XX  
PF 22-JAN-1998; 98FR-0000873.  
XX  
PR 03-OCT-1997; 97FR-0012382.

XX (MERI-) MERIAL SAS.  
XX  
PI Allan G, Chappuis GE, Charreyre CE, Clark E, Ellis J;  
PI Haines D, Harding J, Hassard L, Meehan B;  
XX  
DR WPI; 1999-246948/21.

XX New type II porcine circovirus, used for, e.g. passive immunization  
PT of pregnant sows

PS Claim 14; Fig 1; 48pp; French.

XX The present sequence represents the nucleotide sequence of PCV isolate  
CC Impl011-48121. The specification describes a preparation of type II  
CC porcine circovirus (PCV), which is particularly isolated from a lesion,  
CC from a pig with symptoms of PMWS (porcine multisystemic wasting  
CC syndrome). PCV (attenuated or inactivated), polypeptides derived from  
CC it, and vectors that express these polypeptides are all useful in  
CC vaccines, suitable for administration to adult or young pigs, or to  
CC pregnant sows (for passive immunization of their offspring). DNA  
CC isolated from PCV is used for in vivo or in vitro expression of viral  
CC polypeptides, also as probes or primers for diagnosis in usual  
CC hybridization or amplification assays. These polypeptides may also be  
CC used diagnostically to detect PCV-specific antibodies, while antibodies  
CC raised against the polypeptides can be used to detect antigens, in any  
CC usual immunoassay format.

XX SQ Sequence 1767 BP; 447 A; 360 C; 502 G; 458 T; 0 other;

Query Match 54.4%; Score 381.6; DB 20; Length 1767;



Best Local Similarity 92.0%; Pred. No. 8.6e-170;  
Matches 653; Conservative 0; Mismatches 49; Indels 8; Gaps 2;

QY 1 ATGACGTATCCAAGGAGCGGTTACCGAAGAAGACACCGCCCCCGCAGCCATCTTGGC 60  
|||||  
Db 1749 ATGACGTATCCAAGGAGCGGTTACCGCAGAAGAAGACACCGCCCCCGCAGCCATCTTGGC 1690

QY 61 CAGATCCTCCGCGCGCCCTGGCTCGTCCACCCCGCC-----ACCGTTACCGCTG 113  
|||||  
Db 1689 CAGATCCTCCGCGCGCCCTGGCTCGTCCACCCCGCCCTTCAGAAACCGCTACCGTTG 1630

QY 114 GAGAAGGAAAAATGGCATCTTCAACACCCCGCCTCTCCCGCACCTTCGGATATACTGTCAA 173  
|||||  
Db 1629 GAGAAGGAAAAATGGCATCTTCAACACCCCGCCTCTCCCGCACCTTCGGATATACTGTCAA 1570

QY 174 GCGAACCACAGTCAGAACGCCCTCTCTGGGCGGTGGACATGATGAGATTCAATATTAATGA 233  
|||  
Db 1569 GCGTACCACAGTCACAACGCCCTCTCTGGGCGGTGGACATGATGAGATTTAAATGACGA 1510

QY 234 CTTTCTTCCCCAGAGGGGGGTCAAAACCCCGCTCTGTGCCCCTTTGAATACACAGAAAT 293  
|||  
Db 1509 CTTTGTCCCCGAGAGGGGGGACCAACAAAATCTCTATACCTTTTGAATACTACAGAAAT 1450

QY 294 AAGAAAGGTTAAGGTTGAATTTCTGGCCCTGCTCCCGCATCACCCAGGTTGACAGSGGAGT 353  
|||||  
Db 1449 AAGAAAGGTTAAGGTTGAATTTCTGGCCCTGCTCCCCCATCACCCAGGTTGATAGGGGAGT 1390

QY 354 GGGCTCCAGTGTCTATTTTAGATGATAACTTTGTAAACAAAGGCCACAGCCCTCACCTA 413  
|||||  
Db 1389 GGGCTCCAGTGTCTATTTTAGATGATAACTTTGTAAACAAAGGCCACAGCCCTTAACCTA 1330

QY 414 TGACCCCTATGTAAACTACTCTCTCCGCCATACCATAAACCCAGCCCTTCTCTACCACTC 473  
|||||  
Db 1329 TGACCCCATATGTAAACTACTCTCTCCGCCATACCATAAACCCCTTCTCTACCACTC 1270

QY 474 CCGGTACTTTACCCCAAAACCTGTCTTAGATTTCACCTATTGATTACTTCCAAACCAACAA 533  
|||  
Db 1269 CCGTTACTTTCACACCCCAAAACCTGTCTTGACTCCACTATTGATTACTTCCAAACCAATAA 1210

QY 534 CAAAAGAAACCGTGTGGCTGAGACTACAAACTGCTGGAAATGTAGACCACGTTAGGCCT 593  
|||||  
Db 1209 CAAAAGGAATCAGCTTGGCTGAGGCTACAAACCTCTGGAAATGTGGACCACGTTAGGCCT 1150

QY 594 CGGCACTGCGTTCCGAAAACAGTATATAC-GACCAGGAATACAATATCCGTGTAACCATGT 652  
|||||  
Db 1149 CGGCACTGCGTTCCGAAAACAGTAAATACAGACCAGGACTACAATATCCGTGTAACCATGT 1090

QY 653 ATGTACAATTACAGAGAATTTAATTTTAAAGACCCCCCACTTAACCCCTTAA 702  
|||||  
Db 1089 ATGTACAATTACAGAGAATTTAATCTTAAAGACCCCCCACTTAACCCCTTAA 1040

RESULT 9  
AAX83757/c  
ID AAX83757 standard; DNA; 1361 BP.  
XX  
AC AAX83757;  
XX  
DT 27-AUG-1999 (first entry)  
XX  
DE Porcine circovirus type II B9 nucleotide sequence fragment #2.  
XX  
KW Porcine circovirus type II; PCVII; PCVI; pig; infection; vaccine;  
KW postweaning multisystemic wasting syndrome virus; diagnosis; ds.  
XX  
OS Porcine circovirus.  
XX  
PN W09929717-A2.  
XX  
PD 17-JUN-1999.  
XX  
PF 11-DEC-1998; 98WO-CA01130.  
XX

PR 16-DEC-1997; 97US-0069750.  
PR 11-DEC-1997; 97US-0069233.  
XX  
PA (UYSA-) UNIV SASKATCHEWAN.  
XX  
PI Babiuk LA, Potter AA, Wang L, Willson P;  
XX  
DR WPI; 1999-394957/33.  
XX  
PT New isolated porcine circovirus Type II  
XX  
PS Claim 1; Fig 4; 82pp; English.  
XX  
CC The present invention describes a new isolated porcine circovirus  
CC Type II (PCVII), obtained from postweaning multisystemic wasting  
CC syndrome-affected pigs. AAX83754 to AAX83757 represent PCVII nucleotide  
CC sequences. AAY24929 to AAY24934 represent PCVII open reading frame (ORF)  
CC proteins (N.B. the PCVII ORFs given in Fig 2A to Fig 2B do not  
CC correspond exactly with the PCVII ORFs given in Fig 3A to Fig 3D).  
CC The PCVII polypeptides can be used for treating or preventing PCVII  
CC infection in vertebrates. The products can also be used to detect the  
CC PCVII.  
XX  
SQ Sequence 1361 BP; 334 A; 265 C; 375 G; 387 T; 0 other;

Query Match 84.2%; Score 590.8; DB 20; Length 1361;  
Best Local Similarity 91.5%; Pred. No. 2.1e-168;  
Matches 650; Conservative 0; Mismatches 52; Indels 8; Gaps 2;

QY 1 ATGACGTATCCAAGGAGGCGTTACCGAAGAAGACACCGCCCCCGCAGCCATCTTGGC 60  
|||||  
Db 1324 ATGACGTATCCAAGGAGGCGTTACCGCAGAAGAAGACACCGCCCCCGCAGCCATCTTGGC 1265

QY 61 CAGATCCTCCGCGCGCCCTGGCTCGTCCACCCCGCC-----ACCGTTACCGCTG 113  
|||||  
Db 1264 CAGATCCTCCGCGCGCCCTGGCTCGTCCACCCCGCCCTTCAGAAACCGCTACCGTTG 1205

QY 114 GAGAAGGAAAAATGGCATCTTCAACACCCCGCCTCTCCCGCACCTTCGGATATACTGTCAA 173  
|||||  
Db 1204 GAGAAGGAAAAATGGCATCTTCAACACCCCGCCTCTCCCGCACCTTCGGATATACTGTCAA 1145

QY 174 GCGAACCACAGTCAGAACGCCCTCTCTGGGCGGTGGACATGATGAGATTCAATTAATGA 233  
|||||  
Db 1144 AGCTACCACAGTCACAACGCCCTCTCTGGGCGGTGGACATGATGAGATTAAATGACGA 1085

QY 234 CTTTCTTCCCCAGGAGGGGTCAAAACCCCGCCTCTGTGCCCTTTGAATACTACAGAAAT 293  
|||||  
Db 1084 CTTTGTCTCCCGGAGGGGGACCAACAAAATCTCTATACCTTTTGAATACTACAGAAAT 1025

QY 294 AAGAAAGGTTAAGGTTGAATTTCTGGCCCTGCTCCCGCATCACCCAGGTTGACAGGGGAGT 353  
|||||  
Db 1024 AAGAAAGGTTAAGGTTGAATTTCTGGCCCTGCTCCCCCATCACCCAGGTTGATAGGGGAGT 965

QY 354 GGGCTCCAGTGTCTTATTTTAGATGATAAATTTGTAAACAAAGGCCACAGCCCTCACCTA 413  
|||||  
Db 964 GGGCTCCAGTGTCTTATTTTAGATGATAAATTTGTAAACAAAGGCCACAGCCCTTAACCTA 905

QY 414 TGACCCCTATGTAAACTACTCTCCGCCATACCATAAACCCAGCCCTTCTCTACCACTC 473  
|||||  
Db 904 TGACCCCATATGTAAACTACTCTCCGCCATACCAATCCCCCAACCCCTTCTCTACCACTC 845

QY 474 CCGGTACTTTACCCCAAAACCTGTCTCTAGATTTTCACTATTGATTACTTCCAAACCAACAA 533  
|||||  
Db 844 CCGTTACTTTCACACCCCAAAACCTGTCTTGACTCCACTATTGATTACTTCCAAACCAATAA 785

QY 534 CAAAAGAAACCAAGCTGTGGCTGAGACTACAAACTGCTGGAAATGTAGACCACGTTAGGCCT 593  
|||||  
Db 784 CAAAAGGAATCAGCTTTGGCTGAGGCTACAAACCTCTCTGGAAATGTGGACCACGTTAGGCCT 725

QY 594 CGGCACTGCGTTTCGAAAACAGTATATAC-GACCAGGAATACAATATCCCGTTAACCATGT 652  
|||||  
Db 724 CGGCACTGCGTTTCGAAAACAGTAAATACAGACCAGGACTACAATATCCGTGTAACCATGT 665

Db 1615 AAAAAATGGCATCTTCAACACACCCCGCCTCTCCCGCACCTTCGGATATACTGTCAAGCGTACC 1556  
QY 181 ACAGTCAGAACGCCCTCCTGGCGGGTGACATGATGAGATTCAATATTAATGACTTTCTT 240  
Db 1555 ACAGTCACAACGCCCTCCTGGCGGGTGACATGATGAGATTAAATTGACGACTTTGTT 1496  
QY 241 CCCCCAGGAGGGGTCAAAACCCCGCTCTGTGCCCCCTTGAATACTACAGAATAAGAAAG 300  
Db 1495 CCCCCGAGGGGGACCAACAAATCTCTATACCCCTTGAATACTACAGAATAAGAAAG 1436  
QY 301 GTTAAGTTGAATTCTGGCCCTGCTCCCGGATCACCAGGGTGACAGGGGAGTGGGCTCC 360  
Db 1435 GTTAAGTTGAATTCTGGCCTTGCTCCCCCATCACCCAGGTGATAGGGGAGTGGGCTCC 1376  
QY 361 AGTGCTGTTATTTTAGATGATAAATTTGTAAACAAAGGCCACAGCCCTCACCTATGACCCC 420  
Db 1375 ACTGCTGTTATTTTAGATGATAAATTTGTAAACAAAGGCCACAGCCCTAACCTATGACCCA 1316  
QY 421 TATGTAAACTACTCCTCCGCCATACCATAAACCCAGCCCTTCTCCTACCACCTCCCGGTAC 480  
Db 1315 TATGTAAACTACTCCTCCGCCATACCAATCCCCCAACCCCTTCTCCTACCACCTCCCGTTAC 1256  
QY 481 TTTACCCCCAAACCTGTCTAGATTTCACCTATTGATTACTTCCAAACCAACAAACAAAGA 540  
Db 1255 TTCACACCCAAACCTGTCTTGACTCCACTATTGATTACTTCCAAACCAATAACAAAGG 1196  
QY 541 AACCAGCTGTGGCTGAGACTACAAACTGCTGGAAATGTAGACCACGTAGGCCCTCGGCACT 600  
Db 1195 AATCAGCTTTGGCTGAGCTACAAACCTCTGGAAATGTGGACCACGTAGGCCCTCGGCACT 1136  
QY 601 GCGTTCGAAAACAGTATPACGACGACGAGGAATACAAATATCCGTGTAACCATGTATGTACAA 660  
Db 1135 GCGTTCGAAAACAGTAAATACGACGAGGACTACAATATCCGTGTAACCATGTATGTACAA 1076  
QY 661 TTCAGAGAATTTAATTTTAAAGACCCCCCCTTAACCCCTAA 702  
Db 1075 TTCAGAGAATTTAATCTTAAAGACCCCCCCTTAACCCCTAA 1034

RESULT 6

AAF75841/c  
ID AAF75841 standard; DNA; 1768 BP.  
XX  
AC AAF75841;  
XX  
DT 18-MAY-2001 (first entry)  
DE  
DE PCV DNA fragment of Imp 1121 strain.  
XX  
KW vaccine; pig; myocarditis; abortion; intrauterine infection;  
KW multisystemic wasting syndrome; ds.  
XX  
OS Porcine circovirus-2.  
XX  
PN WO200116330-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 28-AUG-2000; 2000WO-EP08781.  
XX  
PR 31-AUG-1999; 99US-0151564.  
PR 31-MAY-2000; 2000US-0583350.  
XX  
XX (MERI-) MERIAL.  
PA (UYSA-) UNIV SASKATCHEWAN.  
PA (UYBE-) UNIV QUEENS BELFAST.  
XX  
PI Ellis JA, Allan GM, Meehan B, Clark E, Haines D, Hassard L;  
PI Harding J, Charreyre CE, Chappuis GE, Krakowka GS, Audonnet JF;  
PI Mcneilly F;  
XX  
DR WPI; 2001-244408/25.  
XX

PT Use of porcine circovirus-2 immunogen to formulate a vaccine  
PT composition to treat pigs against myocarditis, abortion, intrauterine  
PT infection and/or post-weaning, multisystemic wasting syndrome  
XX associated with PCV-2 -  
PS Claim 11; Fig 7; 134pp; English.  
XX  
CC The present invention relates to the use of porcine circovirus-2 (PCV-2)  
CC immunogen to formulate a vaccine composition to prevent or treat pigs  
CC against myocarditis and/or abortion and/or intrauterine infection and/or  
CC post-weaning, multisystemic wasting syndrome and other pathological  
CC sequelae associated with PCV-2. The present sequence is a DNA fragment of  
CC a strain of PCV, which was used in the present invention.  
XX  
SQ Sequence 1768 BP; 452 A; 359 C; 496 G; 461 T; 0 other;  
  
Query Match 87.9%; Score 617.2; DB 22; Length 1768;  
Best Local Similarity 92.5%; Pred. No. 2.5e-176;  
Matches 649; Conservative 0; Mismatches 53; Indels 0; Gaps 0;  
  
QY 1 ATGACGTATCCAAGGAGGCGTTACCGAAGAAGAGACACCGCCCCCGCAGCCATCTTGGC 60  
Db 1735 ATGACGTATCCAAGGAGGCGTTACCGCAGAGAAGACACCGCCCCCGCAGCCATCTTGGC 1676  
QY 61 CAGATCCTCCGCCCGCCCTGGCTCGTCCACCCCGCCCTTCCGGATATACTGTCAAGCGAAGC 120  
Db 1675 CAGATCCTCCGCCCGCCCTGGCTCGTCCACCCCGCCCTTCCGGATATACTGTCAAGCGTACT 1616  
QY 121 AAAAAATGGCATCTTCAACACACCCGCCCTCTCCCGCACCTTCCGGATATACTGTCAAGCGAAGC 180  
Db 1615 AAAAAATGGCATCTTCAACACACCCGCCCTCTCCCGCACCTTCCGGATATACTGTCAAGCGTACT 1556  
QY 181 ACAGTCAGAACGCCCTCCTGGCGGGTGACATGATGAGATTCAATATTAATGACTTTCTT 240  
Db 1555 ACAGTCACACCGCCCTCCTGGCGGGTGACATGATGAGATTAAATTTGACGACTTTGTT 1496  
QY 241 CCCCCAGGAGGGGGTCAAAACCCCGCTCTGTGCCCTTTGAATACTACAGAATAAGAAAG 300  
Db 1495 CCCCCGAGGGGGGACCAACAAATCTCTATACCCCTTTGAATACTACAGAATAAGAAAG 1436  
QY 301 GTTAAGGTTGAATTTAGATGATAAATTTGTAAACAAAGGCCACAGCCCTCACCTATGACCCC 360  
Db 1435 GTTAAGGTTGAATTTAGATGATAAATTTGTAAACAAAGGCCACAGCCCTAACCTATGACCCA 1376  
QY 361 AGTGCTGTTATTTAGATGATAAATTTGTAAACAAAGGCCACAGCCCTCACCTATGACCCC 420  
Db 1375 ACTGCTGTTATTTAGATGATAAATTTGTAAACAAAGGCCACAGCCCTAACCTATGACCCA 1316  
QY 421 TATGTAAACTACTCCTCCCGCCATACCATAAACCCAGCCCTTCTCCTACCACCTCCCGGTAC 480  
Db 1315 TATGTAAACTACTCCTCCCGCCATACAAATCCCCAACCCCTTCTCCTACCACCTCCCGTTAC 1256  
QY 481 TTTACCCCCAAACCTGTCTTAGATTTTCACTATTGATTACTTCCAAACCAACAAACAAAGA 540  
Db 1255 TTCACACCCAAACCTGTTCTTGACTCCACTATTGATTACTTCCAAACCAATAACAAAGG 1196  
QY 541 AACCAGCTGTGGCTGAGACTACAAACTGCTGGAAATGTAGACCACGTAGGCCCTCGGCACT 600  
Db 1195 AATCAGCTTTGGCTGAGGCTACAAACCTCTAGAAATGTGGACCACGTAGGCCCTCGGCACT 1136  
QY 601 GCGTTCGAAAACAGTATATACGACCAGGAATACAAATATCCGTGTAACCATGTATGTACAA 660  
Db 1135 GCGTTCGAAAACAGTAAATACGACCAGGACTACAATATCCGTGTAACCATGTATGTACAA 1076  
QY 661 TTCAGAGAATTTAATTTTAAAGACCCCCCCTTAACCCCTTAA 702  
Db 1075 TTCAGAGAATTTAATCTTAAAGACCCCCCCTTAACCCCTTAA 1034

RESULT 7

AAF75840/c  
ID AAF75840 standard; DNA; 1768 BP.  
XX





Db 1702 GTTAAGGTGAATTCTGGCCCTGCTCCCCCATCACCCAGGGTGATAGGGAGTGGGCTCC 1761

Qy 361 AGTGCTGTATTTAGATGATAACTTTGTAACAAAGGCCACAGCCCTCACCTATGACCC 420

Db 1762 ACTGCTGTATTTAGATGATAACTTTGTAACAAAGGCCACAGCCCTAACCTATGACCCA 1821

Qy 421 TATGTAACTACTCCTCCGCCATACCATAAACCCAGCCCTTCTCCTACCACTCCCGGTAC 480

Db 1822 TATGTAACTACTCCTCCGCCATACCAATCCCCAACCCCTTCTCCTACCACTCCCGTTAC 1881

Qy 481 TTTACCCCAACCTGTCTAGATTTTCACTATTGATTACTTCCAAACCAACAACAAGA 540

Db 1882 TTCACACCAACCTGTTCTTGACTCCACTATTGATTACTTCCAAACCAACAAGAAGG 1941

Qy 541 AACGAGCTGTGGCTGAGACTACAAACTGCTGGAATGTAGACCAGTAGGCCTCGGCACT 600

Db 1942 AATCAGCTTTGGCTGAGACTACAAACCTCTGGAATGTGGACCACGTAAGGCTCGGCGCT 2001

Qy 601 GCGTTCGAAACAGTATATACGACCAGGAATACAAATATCCGTGTAACCATGTATGTACAA 660

Db 2002 GCGTTCGAAACAGTAAATACGACCAGGACTACAATATCCGTGTAACCATGTATGTACAA 2061

Qy 661 TTCAGAGAAATTAATTTTAAAGACCCCCCACTTAACCCCTAA 702

Db 2062 TTCAGAGAAATTAATCTTAAAGACCCCCCACTTAACCCCTAA 2103

RESULT 3

AAF75830/c

ID AAF75830 standard; DNA; 2769 BP.

XX

AC AAF75830;

XX

DT 18-MAY-2001 (first entry)

XX

DE Plasmid pJP107 DNA fragment.

XX

KW ALVAC; porcine circovirus-2; vaccine; pig; myocarditis; abortion;

KW intrauterine infection; multisystemic wasting syndrome; ds.

XX

OS Unidentified.

XX

PN WO200116330-A2.

XX

PD 08-MAR-2001.

XX

PF 28-AUG-2000; 2000WO-EP08781.

XX

PR 31-AUG-1999; 99US-0151564.

PR 31-MAY-2000; 2000US-0583350.

XX

PA (MERI-) MERIAL.

PA (UYSA-) UNIV SASKATCHEWAN.

PA (UYBE-) UNIV QUEENS BELFAST.

XX

PI Ellis JA, Allan GM, Meehan B, Clark E, Haines D, Hassard L;

PI Harding J, Charreyre CE, Chappuis GE, Krakowka GS, Audonnet JF;

PI Mcneilly F;

XX

DR WPI; 2001-244408/25.

DR P-PSDB; AAB73273.

XX

PT Use of porcine circovirus-2 immunogen to formulate a vaccine

PT composition to treat pigs against myocarditis, abortion, intrauterine

PT infection and/or post-weaning, multisystemic wasting syndrome

PT associated with PCV-2 -

XX

PS Example 3 #3; Fig 6 #1; 134pp; English.

XX

CC The present invention relates to the use of porcine circovirus-2 (PCV-2)

CC immunogen to formulate a vaccine composition to prevent or treat pigs

CC against myocarditis and/or abortion and/or intrauterine infection and/or

CC post-weaning, multisystemic wasting syndrome and other pathological

CC sequalae associated with PCV-2. The present sequence is a DNA fragment of

CC a plasmid, which expresses gene products of PCV-2.

XX

SQ Sequence 2769 BP; 828 A; 455 C; 538 G; 948 T; 0 other;

Query Match 88.6%; Score 622; DB 22; Length 2769;

Best Local Similarity 92.9%; Pred. No. 1.1e-177;

Matches 652; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 ATGACGTATCCAAGGAGCGTTACCGAAGAAGACACCGCCCGCAGCCATCTTGGC 60

Db 1898 ATGACGTATCCAAGGAGCGTTACCGAAGAAGACACCGCCCGCAGCCATCTTGGC 1839

QY 61 CAGATCCTCCGCCCGCCCTGGCTCGTCCACCCCGCCACCGTTACCGCTGGAGAAGG 120

Db 1838 CAGATCCTCCGCCCGCCCTGGCTCGTCCACCCCGCCACCGTTACCGCTGGAGAAGG 1779

QY 121 AAAAAATGGCATCTTCAACACCCGCCCTCTCCCGCACCTTCGGGATATACTGTCAAGCGAACC 180

Db 1778 AAAAAATGGCATCTTCAACACCCGCCCTCTCCCGCACCTTCGGGATATACTGTCAAGCGTACC 1719

QY 181 ACAGTCAGAAACGCCCTCCTGGCGGTGGACATGATGAGATTCAATTAATGACTTCTT 240

Db 1718 ACAGTCAGAAACGCCCTCCTGGCGGTGGACATGATGAGATTCAATTAATGACTTCTT 1659

QY 241 CCCCCAGGAGGGGGTCAAAACCCCGCTCTGTGCCCTTTGAATACTACAGAATAAGAAAG 300

Db 1658 CCCCCAGGAGGGGGTCAAAACCCCGCTCTGTGCCCTTTGAATACTACAGAATAAGAAAG 1599

QY 301 GTTAAAGGTTGAATTCTGGCCCTGCTCCCGCATCACCCAGGGTGACAGGGGAGTGGGCTCC 360

Db 1598 GTTAAAGGTTGAATTCTGGCCCTGCTCCCGCATCACCCAGGGTGATAGGGGAGTGGGCTCC 1539

QY 361 AGTGCTGTATTTAGATGATAACTTTGTAACAAAGGCCACAGCCCTCACCTATGACCC 420

Db 1538 ACTGCTGTATTTAGATGATAACTTTGTAACAAAGGCCACAGCCCTCACCTATGACCC 1479

QY 421 TATGTAAACTACTCCTCCGCCATACCATAAACCCAGCCCTTCTCCTACCACTCCCGGTAC 480

Db 1478 TATGTAAACTACTCCTCCGCCATACCAATCCCCAACCCCTTCTCCTACCACTCCCGGTAC 1419

QY 481 TTTACCCCCAAACCTGTCTCTAGATTTCACATATTGATTACTTCCAAACCAACAACAAGA 540

Db 1418 TTCACACCCAAACCTGTCTCTAGATTTCACATATTGATTACTTCCAAACCAACAACAAGA 1359

QY 541 AACCCAGCTGTGGCTGAGACTACAAACTGCTGGAATGTAGACCAGTAGGCCTCGGCACT 600

Db 1358 AATCAGCTTTGGCTGAGACTACAAACCTCTGGAATGTGGACCACGTAGGCCTCGGCGCT 1299

QY 601 GCGTTCGAAACAGTATATACGACCAGGAATACAATATCCGTGTAACCATGTATGTACAA 660

Db 1298 GCGTTCGAAACAGTAAATACGACCAGGACTACAATATCCGTGTAACCATGTATGTACAA 1239

QY 661 TTCAGAGAAATTTAATTTTAAAGACCCCCCACTTAACCCCTTAA 702

Db 1238 TTCAGAGAAATTTAATCTTAAAGACCCCCCACTTAACCCCTTAA 1197

RESULT 4

AAF28320/c

ID AAF28320 standard; DNA; 3609 BP.

XX

AC AAF28320;

XX

DT 30-MAR-2001 (first entry)

XX

DE pJP107 donor plasmid for PCV2 ORF2 and ORF1.

XX

KW PCV2; porcine circovirus 2; virucide; immunostimulant; vaccine;

KW postweaning multisystemic wasting syndrome; PMWS; infection;

KW pig pathogen; open reading frame; ORF; ss.

XX

OS Porcine circovirus type 2.



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2003, 09:05:58 ; Search time 251 Seconds  
(without alignments)  
6298.418 Million cell updates/sec

Title: US-09-514-245B-25  
Perfect score: 702  
Sequence: 1 atgacgtatccaaggaggcg.....acccccacttaacccttaa 702

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	622	88.6	2520	22 AAF75827	Plasmid pJP102 DNA
2	622	88.6	2520	22 AAF28317	pJP102 donor plasm
C 3	622	88.6	2769	22 AAF75830	Plasmid pJP107 DNA
C 4	622	88.6	3609	22 AAF28320	pJP107 donor plasm
C 5	620.4	88.4	1768	20 AAX83754	Porcine circovirus
C 6	617.2	87.9	1768	22 AAF75841	PCV DNA fragment o
C 7	612.4	87.2	1768	22 AAF75840	PCV DNA fragment o
C 8	595.6	84.8	1786	20 AAX83755	Porcine circovirus
C 9	590.8	84.2	1361	20 AAX83757	Porcine circovirus

C 10	381.6	54.4	1767	20 AAX35378	Nucleotide sequenc
C 11	381.6	54.4	1767	20 AAX35210	Nucleotide sequenc
C 12	381.6	54.4	1767	21 AA256869	DNA sequence of PC
C 13	381.6	54.4	1767	22 AAF75835	PCV DNA fragment o
C 14	378.4	53.9	1767	20 AAX35379	Nucleotide sequenc
C 15	378.4	53.9	1767	20 AAX35211	Nucleotide sequenc
C 16	378.4	53.9	1767	21 AA256870	DNA sequence of PC
C 17	378.4	53.9	1767	22 AAF75836	PCV DNA fragment o
C 18	340	48.4	1768	20 AAX35380	Nucleotide sequenc
C 19	340	48.4	1768	20 AAX35381	Nucleotide sequenc
C 20	340	48.4	1768	20 AAX35213	Nucleotide sequenc
C 21	340	48.4	1768	20 AAX35212	Nucleotide sequenc
C 22	340	48.4	1768	21 AA256871	DNA sequence of PC
C 23	340	48.4	1768	21 AA256872	DNA sequence of PC
C 24	340	48.4	1768	22 AAF75837	PCV DNA fragment o
C 25	340	48.4	1768	22 AAF75838	PCV DNA fragment o
C 26	339	48.3	1768	20 AAX35382	Nucleotide sequenc
C 27	339	48.3	1768	20 AAX35012	Genomic DNA sequen
C 28	339	48.3	1768	20 AAX35214	Nucleotide sequenc
C 29	311	44.3	1759	20 AAX85593	Nucleotide sequenc
C 30	307.8	43.8	1759	20 AAX87992	Porcine circovirus
C 31	273.4	38.9	7460	22 AAH74867	Nucleotide sequenc
C 32	256.4	36.5	5285	22 AAH74865	Nucleotide sequenc
C 33	256.4	36.5	5650	22 AAH74866	Nucleotide sequenc
C 34	203.6	29.0	1759	20 AAX35013	Nucleotide sequen
C 35	199.4	28.4	1759	22 AAF75839	DNA fragment of PK
C 36	44.6	6.4	4403765	22 AAI99683	Mycobacterium tube
C 37	44.6	6.4	4411529	22 AAI99682	Mycobacterium tube
C 38	44.4	6.3	953	24 ABQ37014	Oligonucleotide fo
C 39	44.4	6.3	953	24 ABQ37015	Oligonucleotide fo
C 40	44	6.3	1181	23 ABL24269	Drosophila melanog
C 41	44	6.3	4905	23 ABL24268	Drosophila melanog
C 42	43.4	6.2	10348	22 ABA08714	Human Huntington's
C 43	42.6	6.1	592	21 AA293361	Sequence encoding
C 44	41.8	6.0	322	18 AAT75508	P. americanus anti
C 45	41.8	6.0	322	21 AA249961	Winter flounder li

ALIGNMENTS

RESULT 1  
AAAF75827  
ID AAF75827 standard; DNA; 2520 BP.  
XX  
AC AAF75827;  
XX  
DT 18-MAY-2001 (first entry)  
XX  
DE Plasmid pJP102 DNA fragment.  
XX  
KW ALVAC; porcine circovirus-2; vaccine; pig; myocarditis; abortion;  
KW intrauterine infection; multisystemic wasting syndrome; ds.  
XX  
OS Unidentified.  
XX  
PN WO200116330-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 28-AUG-2000; 2000WO-EP08781.  
XX  
PR 31-AUG-1999; 99US-0151564.  
PR 31-MAY-2000; 2000US-0583350.  
XX  
PA (MERI-) MERIAL.  
PA (UYSA-) UNIV SASKATCHEWAN.  
PA (UYBE-) UNIV QUEENS BELFAST.  
XX  
PI Ellis JA, Allan GM, Meehan B, Clark E, Haines D, Hassard L;  
PI Harding J, Charreyre CE, Chappuis GE, Krakowka GS, Audonnet JF;  
PI Mcneilly F;  
XX



WPI; 2001-244408/25.  
P-PSDB; AAB73272.

Use of porcine circovirus-2 immunogen to formulate a vaccine composition to treat pigs against myocarditis, abortion, intrauterine infection and/or post-weaning, multisystemic wasting syndrome associated with PCV-2

Example 2 #3; Fig 3 #1; 134pp; English.

The present invention relates to the use of porcine circovirus-2 (PCV-2) immunogen to formulate a vaccine composition to prevent or treat pigs against myocarditis and/or abortion and/or intrauterine infection and/or post-weaning, multisystemic wasting syndrome and other pathological sequelae associated with PCV-2. The present sequence is a DNA fragment of a plasmid, which expresses gene products of PCV-2.

Sequence 2520 BP; 777 A; 482 C; 382 G; 879 T; 0 other;

Query Match 88.6%; Score 622; DB 22; Length 2520;  
Best Local Similarity 92.9%; Pred. No. 1e-177;  
Matches 652; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

1 ATGACGTATCCAAGGAGCGGTTACCGAAGAAGACACCGCCCCCGCAGCCATCTTGGC 60  
|||||  
1402 ATGACGTATCCAAGGAGCGGTTACCGCAGAGAAGACACCGCCCCCGCAGCCATCTTGGC 1461

61 CAGATCCTCCGCGCGCCCTGGCTCGTCCACCCCGCCACCGTTACCGCTGGAGAAGG 120  
|||||  
1462 CAGATCCTCCGCGCGCCCTGGCTCGTCCACCCCGCCACCGTTACCGCTGGAGAAGG 1521

121 AAAAATGGCATCTCAACACCCCGCTCTCCCGACCTTCGGATATACTGTCAAGCGAACC 180  
|||||  
1522 AAAAATGGCATCTCAACACCCCGCTCTCCCGACCTTCGGATATACTGTCAAGCGTACC 1581

181 ACAGTCAGAACGGCCTCCTGGCGGTGGACATGATGAGATTCAATATTAATGACTTTCTT 240  
|||||  
1582 ACAGTCACAACGCCCTCCTGGCGGTGGACATGATGAGATTAAATTTGACGACTTTGTT 1641

241 CCCCCAGGAGGGGTCAAAACCCCGCTCTGTGCCCTTTGAATACTACAGAATAAGAAAG 300  
|||||  
1642 CCCCCGAGGGGGACCAACAAATCTCTATACCCTTTGAATACTACAGAATAAGAAAG 1701

301 GTTAAGGTTGAATTTGGCCCTGTCTCCCGCATCACCCAGGGTGACAGGGGAGTGGGCTCC 360  
|||||  
1702 GTTAAGGTTGAATTTGGCCCTGTCTCCCGCATCACCCAGGGTGATAGGGGAGTGGGCTCC 1761

361 AGTGCTGTTATTTAGATGATAAATTTGTAAAGGCCACAGCCCTCACCTATGACCCCC 420  
|||||  
1762 ACTGCTGTTATTTAGATGATAAATTTGTAAAGGCCACAGCCCTAACCTATGACCCCA 1821

421 TATGTAACTACTCCTCCGCCATACCATACCCAGCCCTTCTCCTACCACTCCCGGTAC 480  
|||||  
1822 TATGTAACTACTCCTCCGCCATACAAATCCCCCAACCTTCTCCTACCACTCCCGGTAC 1881

481 TTTACCCCCAAACCTGTCTCTAGATTTCACATATTGATTACTTCCAAACCAACAAAGA 540  
|||||  
1882 TTCACACCCCAACCTGTCTTGAATCTTGAATTTGATTACTTCCAAACCAATAACAAAGG 1941

541 AACCAGCTGTGGCTGAGACTACAAACTGCTGGAAATGTAGACCACGTAGGCTCGGCACT 600  
|||||  
1942 AATCAGCTTTGGCTGAGACTACAAACCTCTGGAAATGTGGACCACGTAGGCTCGGCGCT 2001

601 GCGTTCGAAACAGTATATACGACCGAGGAATACAAATATCCGTGTAAACCATGTATGTACAA 660  
|||||  
2002 GCGTTCGAAACAGTAAATACGACCGAGGACTACAAATATCCGTGTAAACCATGTATGTACAA 2061

661 TTCAGAGAAATTTAATTTTAAAGACCCCCCACTTAACCCCTTAA 702  
|||||  
2062 TTCAGAGAAATTTAATCTTAAAGACCCCCCACTTAACCCCTTAA 2103

AAF28317  
ID AAF28317 standard; DNA; 2520 BP.  
XX  
AC AAF28317;  
XX  
DT 30-MAR-2001 (first entry)  
XX  
DE pJP102 donor plasmid for PCV2 ORF2.  
XX  
KW PCV2; porcine circovirus 2; virucide; immunostimulant; vaccine;  
KW postweaning multisystemic wasting syndrome; PMWS; infection;  
KW pig pathogen; open reading frame 2; ORF2; ss.  
XX  
OS Porcine circovirus type 2.  
OS Synthetic.  
XX  
PN WO200077216-A2.  
XX  
XX 21-DEC-2000.  
PD  
XX 09-JUN-2000; 2000WO-IB00882.  
PF  
XX 10-JUN-1999; 99US-0138478.  
PR  
PR 01-JUN-2000; 2000US-0583545.  
XX  
PA (MERI-) MERIAL.  
XX  
PI Bublot M, Perez JM, Charreyre CE;  
XX  
DR WPI; 2001-080692/09.  
DR P-PSDB; AAB61154.  
XX  
PT Novel recombinant virus comprising DNA from porcine circovirus 2 useful  
PT as vaccine for treatment and prophylaxis of porcine circovirus  
PT infection, such as postweaning multisystemic wasting syndrome in pigs  
PT  
XX  
PS Example 2; Fig 3; 60pp; English.  
XX  
CC The present sequence was used in the construction of a recombinant  
CC virus comprising DNA from porcine circovirus 2 (PCV2). The  
CC recombinant virus is useful as vaccine for treatment and prophylaxis of  
CC PCV2 infection, such as postweaning multisystemic wasting syndrome (PMWS)  
CC in young pigs.  
XX  
SQ Sequence 2520 BP; 777 A; 482 C; 382 G; 879 T; 0 other;

Query Match 88.6%; Score 622; DB 22; Length 2520;  
Best Local Similarity 92.9%; Pred. No. 1e-177;  
Matches 652; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

1 ATGACGTATCCAAGGAGCGGTTACCGAAGAAGACACCGCCCCCGCAGCCATCTTGGC 60  
|||||  
1402 ATGACGTATCCAAGGAGCGGTTACCGCAGAGAAGACACCGCCCCCGCAGCCATCTTGGC 1461

61 CAGATCCTCCGCGCGCCCTGGCTCGTCCACCCCGCCACCGTTACCGCTGGAGAAGG 120  
|||||  
1462 CAGATCCTCCGCGCGCCCTGGCTCGTCCACCCCGCCACCGTTACCGCTGGAGAAGG 1521

121 AAAAATGGCATCTTCAACACCCCGCTCTCCCGACCTTCGGATATACTGTCAAGCGAACC 180  
|||||  
1522 AAAAATGGCATCTTCAACACCCCGCTCTCCCGACCTTCGGATATACTGTCAAGCGTACC 1581

181 ACAGTCAGAACGCCCTCCTGGCGGTGGACATGATGAGATTCAATATTAATGACTTTCTT 240  
|||||  
1582 ACAGTCACAACGCCCTCCTGGCGGTGGACATGATGAGATTAAATTTGACGACTTTGTT 1641

241 CCCCCAGGAGGGGGTCAAAACCCCGCTCTGTGCCCTTTGAATACTACAGAATAAGAAAG 300  
|||||  
1642 CCCCCGAGGGGGGACCAACAAATCTCTATACCCTTTGAATACTACAGAATAAGAAAG 1701

301 GTTAAGGTTGAATTTGGCCCTGTCTCCCGCATCACCCAGGGTGACAGGGGAGTGGGCTCC 360  
|||||  
1702 GTTAAGGTTGAATTTGGCCCTGTCTCCCGCATCACCCAGGGTGATAGGGGAGTGGGCTCC 1761

361 AGTGCTGTTATTTAGATGATAAATTTGTAAAGGCCACAGCCCTCACCTATGACCCCC 420  
|||||  
1762 ACTGCTGTTATTTAGATGATAAATTTGTAAAGGCCACAGCCCTAACCTATGACCCCA 1821

421 TATGTAACTACTCCTCCGCCATACCATACCCAGCCCTTCTCCTACCACTCCCGGTAC 480  
|||||  
1822 TATGTAACTACTCCTCCGCCATACAAATCCCCCAACCTTCTCCTACCACTCCCGGTAC 1881

481 TTTACCCCCAAACCTGTCTCTAGATTTCACATATTGATTACTTCCAAACCAACAAAGA 540  
|||||  
1882 TTCACACCCCAACCTGTCTTGAATCTTGAATTTGATTACTTCCAAACCAATAACAAAGG 1941

541 AACCAGCTGTGGCTGAGACTACAAACTGCTGGAAATGTAGACCACGTAGGCTCGGCACT 600  
|||||  
1942 AATCAGCTTTGGCTGAGACTACAAACCTCTGGAAATGTGGACCACGTAGGCTCGGCGCT 2001

601 GCGTTCGAAACAGTATATACGACCGAGGAATACAAATATCCGTGTAAACCATGTATGTACAA 660  
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2002 GCGTTCGAAACAGTAAATACGACCGAGGACTACAAATATCCGTGTAAACCATGTATGTACAA 2061

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; LENGTH: 1768
; TYPE: DNA
; ORGANISM: Porcine circovirus
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)..(1768)
; OTHER INFORMATION: N represents A or C or G or T
US-09-082-558-6

Query Match      48.3%; Score 339; DB 4; Length 1768;
Best Local Similarity 92.2%; Pred. No. 9.4e-96;
Matches 357; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

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QY 376 GATGATAACTTTGTAACAAAGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTCC 435
Db 1708 GATGATAACTTTGTAACAAAGGCCACAGCCCTAACCTATGACCCATATGTAAACTACTCC 1649

QY 436 TCCCGCCATACCAATAACCCAGCCCTTCTCCTACCACTCCCGGTACTTTACCCCAACCT 495
Db 1648 TCCCGCCATACCAATAACCCCAACCCCTTCTCCTACCACTCCCGGTACTTTACCAACCT 1589

QY 496 GTCCTAGATTTCACCTATTGATTACTTCCAAACCAACAAAGAAAGAACCCAGCTGGGCTG 555
Db 1588 GTTCTTGACTCCACTATTGATTACTTCCAAACCAATAACAAAGGAATCAGCTTTGGCTG 1529

QY 556 AGACTACAAACTGCTGGAAATGTAGACCACGTTAGCCCTCGGCACTGCGTTTCGAAACAGT 615
Db 1528 AGGCTACAAACCTTGTAGAAATGTGGACCACGTTAGCCCTCGGCACTGCGTTTCGAAACAGT 1469

QY 616 ATATACGACCAGGATACAAATATCCGTGTAAACCATGTATGTACAAATTCAGAGAAATTAAT 675
Db 1468 ATATACGACCAGGACTACAAATATCCGTGTAAACCATGTATGTACAAATTCAGAGAAATTAAT 1409

QY 676 TTAAAGACCCCCCACTTAACCCCTTAA 702
Db 1408 CTAAAGACCCCCCACTTAACCCCTTAA 1382
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```
RESULT 14
US-09-161-092-6/c
; Sequence 6, Application US/09161092
; Patent No. 6391314
; GENERAL INFORMATION:
; APPLICANT: ALLAN, Gordon
; APPLICANT: MEEHAN, Brian
; APPLICANT: CLARK, Edward
; APPLICANT: HAINES, Deborah
; APPLICANT: HASSARD, Lori
; APPLICANT: HARDING, John
; APPLICANT: CHARREYRE, Catherine E.
; APPLICANT: CHAPPUIS, Gilles E.
; TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC
; TITLE OF INVENTION: REAGENTS
; FILE REFERENCE: ALLAN
; CURRENT APPLICATION NUMBER: US/09/161,092
; CURRENT FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/082,558
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 9800873
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 9803707
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 97/12382
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 6
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; TYPE: DNA
; ORGANISM: Porcine circovirus
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)..(1768)
; OTHER INFORMATION: N represents A or C or G or T
US-09-161-092-6

Query Match      48.3%; Score 339; DB 4; Length 1768;
Best Local Similarity 92.2%; Pred. No. 9.4e-96;
Matches 357; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 316 TGGCCCTGCTCCCGATCACCCAGGGTGACAGGGGAGTGGGCTCCAGTGGTATTATTA 375
Db 1768 TGGCCCTGCTCCCGATCACCCAGGGTGATAGGGGAGTGGGCTCCAGTGGTATTATTA 1709

QY 376 GATGATAACTTTGTAACAAAGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTCC 435
Db 1708 GATGATAACTTTGTAACAAAGGCCACAGCCCTAACCTATGACCCATATGTAAACTACTCC 1649

QY 436 TCCCGCCATACCAATAACCCAGCCCTTCTCCTACCACTCCCGGTACTTTACCCCAACCT 495
Db 1648 TCCCGCCATACCAATAACCCCAACCCCTTCTCCTACCACTCCCGGTACTTTACCAACCT 1589

QY 496 GTCCTAGATTTCACCTATTGATTACTTCCAAACCAACAAAGAAAGAACCCAGCTGGGCTG 555
Db 1588 GTTCTTGACTCCACTATTGATTACTTCCAAACCAATAACAAAGGAATCAGCTTTGGCTG 1529

QY 556 AGACTACAAACTGCTGGAAATGTAGACCACGTTAGCCCTCGGCACTGCGTTTCGAAACAGT 615
Db 1528 AGGCTACAAACCTTGTAGAAATGTGGACCACGTTAGCCCTCGGCACTGCGTTTCGAAACAGT 1469

QY 616 ATATACGACCAGGATACAAATATCCGTGTAAACCATGTATGTACAAATTCAGAGAAATTAAT 675
Db 1468 ATATACGACCAGGACTACAAATATCCGTGTAAACCATGTATGTACAAATTCAGAGAAATTAAT 1409

QY 676 TTAAAGACCCCCCACTTAACCCCTTAA 702
Db 1408 CTAAAGACCCCCCACTTAACCCCTTAA 1382
```

```
RESULT 15
US-09-267-177-24
; Sequence 24, Application US/09267177
; Patent No. 6287856
; GENERAL INFORMATION:
; APPLICANT: Poet, Steven E.
; APPLICANT: Ritchie, Branson W.
; APPLICANT: Niagro, Frank D.
; APPLICANT: Lukert, Phil D.
; TITLE OF INVENTION: Vaccines against Circovirus Infections
; FILE REFERENCE: 21099.0057
; CURRENT APPLICATION NUMBER: US/09/267,177
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: 60/077,890
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 699
; TYPE: DNA
; ORGANISM: porcine circovirus
US-09-267-177-24
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Query Match      43.8%; Score 307.8; DB 4; Length 699;
Best Local Similarity 67.0%; Pred. No. 3e-86;
Matches 470; Conservative 0; Mismatches 222; Indels 9; Gaps 2;

QY 1 ATGACGTATCCAAGGAGCGGTTACCGAAGAAGACACCGCCCGCAGCATCTTGGC 60
Db 1 ATGACGTGGCCCAAGGAGCGGTTACCGCAGAAGAAGACCGCCCGCAGCATCTTGA 60
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QY	61	CAGATCCTCCGCGCGCCCTGGCTCGTCCACCC-----CCGCCACCGTTACCGCTGG	114
Db			
QY	61	AACATCCTCCGAGAGACCAATATTGGCACACCCCGCTTCAGAAACCGTTACAGATGG	120
Db			
QY	115	AGAAAGGAAAAATGGCATCTTCAACACCCCGCTCTCCCGCACCTTCGGATATACTGTCAAG	174
Db			
QY	121	CGCCGAAAGACGGGTATCTTCAATTCCCGCCTTTCTACAGAATTGTACTCACCATAAAA	180
Db			
QY	175	CGAACACACAGTCAGAACGCCCTCCTGGCGGTGGACATGATGAGATTCAATATTAATGAC	234
Db			
QY	181	GGA--GGATACTCGCAGCCCATCTTGGAATGTTAACTACCTCAAAATTCACATCGGCCAG	237
Db			
QY	235	TTTCTTCCCCCAGGAGGGGTCAAAACCCCGCTCTGTGCCCTTTGAATACTACAGAATA	294
Db			
QY	238	TTCTCCCCCCTCAGCGGCGCAACCCCTACCCCTACCTTCCAATACTACCGTATT	297
Db			
QY	295	AGAAAGGTTAAGTTGAATTCTGGCCCTGTCTCCCGATCACCCAGGGTGACAGGGGAGTG	354
Db			
QY	298	AGAAAGGCTAAATATGAATTTTACCCCGAGAGACCCCATCACCTCTAATCAAAGAGGTGT	357
Db			
QY	355	GGCTCCAGTGTGTTATTTAGATGATAAATTGTGAACAAAGCCACAGCCCTCACCTAT	414
Db			
QY	358	GGTCCACTGTTGTTATCTTGGATGCCAACTTTGTAACCCCTCCACCAACTTGGCCTAT	417
Db			
QY	415	GACCCCTATGTAAACTACTCTCCCGCCATACCATAAACCCAGCCCTTCTCCTACCCTCC	474
Db			
QY	418	GACCCCTATATTAACACTACTCTCCCGCCACACCATAGGAGCCCTTTACCTACCCTCC	477
Db			
QY	475	CGGTACTTTACCCCAAACCTGTCTCTAGATTTTCACTATTGATTACTTCCAAACCAAC	534
Db			
QY	478	AGGTACTTCACCCCAAACCTGAGCTGGACCAACAATGATTTGGTTCCACCCCAATAAT	537
Db			
QY	535	AAAAGAAACCAAGCTGTGGCTGAGACTACAAACTGCTGGAATGTAGACCAACGTAGGCCTC	594
Db			
QY	538	AAAAGAAACCAAGCTGTGGCTCCATTTAAATACCCACACCAATGTGAGCACACAGGCCTC	597
Db			
QY	595	GGCACTGCGTTCGAAAAACAGTATATACGACCAGGAATACAATATCCGTGTAACCATGTAT	654
Db			
QY	598	GGCTATGCGCTCCAAAATGCAGCCACAGCCCCAAAATTATGTGGTAAGGCTGACTATTAT	657
Db			
QY	655	GTACAATTCAGAGAATTTTAATTTTAAAGACCCCCCACTTAA	695
Db			
QY	658	GTACAATTCAGAGAATTTATCCTTAAAGACCCCTCTAAATAA	698
Db			

Db 1408 TCTTAAAGACCCCGCCACTTAAACCCCTAA 1381

RESULT 9

US-09-082-558-3/c

; Sequence 3, Application US/09082558A

; Patent No. 6368601

; GENERAL INFORMATION:

; APPLICANT: ALLAN, Gordon

; APPLICANT: MEEHAN, Brian

; APPLICANT: CLARK, Edward

; APPLICANT: HAINES, Deborah

; APPLICANT: HASSARD, Lori

; APPLICANT: HARDING, John

; APPLICANT: CHARREYRE, Catherine E.

; APPLICANT: CHAPPUIS, Gilles E.

; TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC

; TITLE OF INVENTION: REAGENTS

; FILE REFERENCE: ALLAN

; CURRENT APPLICATION NUMBER: US/09/082,558A

; CURRENT FILING DATE: 1998-05-21

; EARLIER APPLICATION NUMBER: FR 9800873

; EARLIER FILING DATE: 1998-01-22

; EARLIER APPLICATION NUMBER: FR 9803707

; EARLIER FILING DATE: 1998-03-20

; EARLIER APPLICATION NUMBER: FR 97/12382

; EARLIER FILING DATE: 1997-10-03

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 1768

; TYPE: DNA

; ORGANISM: Porcine circovirus

US-09-082-558-3

Query Match 48.4%; Score 340; DB 4; Length 1768;

Best Local Similarity 92.3%; Pred. No. 4.6e-96;

Matches 358; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 315 CTGGCCCTGCTCCCGCATCACCCAGGGTGACAGGGGAGTGGGCTCCAGTGCTGTATTATT 374

Db 1768 CTGGCCCTGCTCCCGCATCACCCAGGGTGATAGGGGAGTGGGCTCCACTGCTGTATTCT 1709

QY 375 AGATGATAACTTTGTAACAAAGGCCACAGCCCTTCTCCTACCACTCCCGGTACTTTACCCCAAAACC 434

Db 1708 AGATGATAACTTTGTAACAAAGGCCACAGCCCTTACCTATGACCCCATATGTAAACTACTC 1649

QY 435 CTCCCGCCATACCAACCCAGCCCTTCTCCTACCACTCCCGGTACTTTACCCCAAAACC 494

Db 1648 CTCCCGCCATACAAATCCCAACCCCTTCTCCTACCACTCCCGGTACTTCCACCCCAAAACC 1589

QY 495 TGTCTAGATTTCATATTGATTACTTCCAACCAACAAACAAAGAAACCAGCTGTGGCT 554

Db 1588 TGTCTTGACTCCACTATTGATTACTTCCAACCAACAAACAAAGGAATCAGCTTTGGCT 1529

QY 555 GAGACTACAAACTGCTGGAAATGTAGACCACGTAGGCCCTCGGCACCTGCGTTTCGAAACAG 614

Db 1528 GAGGCTACAAACCTCTAGAAATGTGGACCACGTAGGCCCTCGGCACCTGCGTTTCGAAACAG 1469

QY 615 TATATACGACCAAGGAATACAATATCCGTGTAAACCATGTATGTACAATTCAGAGAAATTAA 674

Db 1468 TATATACGACCAAGGAATACAATATCCGTGTAAACCATGTATGTACAATTCAGAGAAATTAA 1409

QY 675 TTTTAAAGACCCCGCCACTTAACCCCTTAA 702

Db 1408 TCTTAAAGACCCCGCCACTTAAACCCCTAA 1381

RESULT 10

US-09-082-558-4/c

; Sequence 4, Application US/09082558A

; Patent No. 6368601

; GENERAL INFORMATION:

; APPLICANT: ALLAN, Gordon

; APPLICANT: MEEHAN, Brian

; APPLICANT: CLARK, Edward

; APPLICANT: HAINES, Deborah

; APPLICANT: HASSARD, Lori

; APPLICANT: HARDING, John

; APPLICANT: CHARREYRE, Catherine E.

; APPLICANT: CHAPPUIS, Gilles E.

; TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC

; TITLE OF INVENTION: REAGENTS

; FILE REFERENCE: ALLAN

; CURRENT APPLICATION NUMBER: US/09/082,558A

; CURRENT FILING DATE: 1998-05-21

; EARLIER APPLICATION NUMBER: FR 9800873

; EARLIER FILING DATE: 1998-01-22

; EARLIER APPLICATION NUMBER: FR 9803707

; EARLIER FILING DATE: 1998-03-20

; EARLIER APPLICATION NUMBER: FR 97/12382

; EARLIER FILING DATE: 1997-10-03

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 1768

; TYPE: DNA

; ORGANISM: Porcine circovirus

US-09-082-558-4

Query Match 48.4%; Score 340; DB 4; Length 1768;

Best Local Similarity 92.3%; Pred. No. 4.6e-96;

Matches 358; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 315 CTGGCCCTGCTCCCGCATCACCCAGGGTGACAGGGGAGTGGGCTCCAGTGCTGTATTATT 374

Db 1768 CTGGCCCTGCTCCCGCATCACCCAGGGTGATAGGGGAGTGGGCTCCACTGCTGTATTCT 1709

QY 375 AGATGATAACTTTGTAACAAAGGCCACAGCCCTTCTCCTACCACTCCCGGTACTTTACCCCAAAACC 434

Db 1708 AGATGATAACTTTGTAACAAAGGCCACAGCCCTTAAACCTATGACCCCATATGTAAACTACTC 1649

QY 435 CTCCCGCCATACCAACCCAGCCCTTCTCCTACCACTCCCGGTACTTTACCCCAAAACC 494

Db 1648 CTCCCGCCATACAAATCCCAACCCCTTCTCCTACCACTCCCGGTACTTCCACCCCAAAACC 1589

QY 495 TGTCTAGATTTCATATTGATTACTTCCAACCAACAAACAAAGAAACCAGCTGTGGCT 554

Db 1588 TGTCTTGACTCCACTATTGATTACTTCCAACCAACAAACAAAGGAATCAGCTTTGGCT 1529

QY 555 GAGACTACAAACTGCTGGAAATGTAGACCACGTAGGCCCTCGGCACCTGCGTTTCGAAACAG 614

Db 1528 GAGACTACAAACCTCTGGAAATGTGGACCACGTAGGCCCTCGGCACCTGCGTTTCGAAACAG 1469

QY 615 TATATACGACCAAGGAATACAATATCCGTGTAAACCATGTATGTACAATTCAGAGAAATTAA 674

Db 1468 TAAATACGACCAAGGACTACAATATCCGTGTAAACCATGTATGTACAATTCAGAGAAATTAA 1409

QY 675 TTTTAAAGACCCCGCCACTTAACCCCTTAA 702

Db 1408 TCTTAAAGACCCCGCCACTTAAACCCCTTAA 1381

RESULT 11

US-09-161-092-3/c

; Sequence 3, Application US/09161092

; Patent No. 6391314

; GENERAL INFORMATION:

; APPLICANT: ALLAN, Gordon

; APPLICANT: MEEHAN, Brian

; APPLICANT: CLARK, Edward

; APPLICANT: HAINES, Deborah

; APPLICANT: HASSARD, Lori

; APPLICANT: HARDING, John

; APPLICANT: CHARREYRE, Catherine E.



; APPLICANT: CHAPPUIS, Gilles E.  
; TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC  
; FILE REFERENCE: REAGENTS  
; CURRENT APPLICATION NUMBER: US/09/161,092  
; CURRENT FILING DATE: 1998-09-25  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/082,558  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 9800873  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-22  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 9803707  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 97/12382  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-03  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 1768  
; TYPE: DNA  
; ORGANISM: Porcine circovirus  
US-09-161-092-3

Query Match 48.4%; Score 340; DB 4; Length 1768;  
Best Local Similarity 92.3%; Pred. No. 4.6e-96;  
Matches 358; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 315 CTGGCCCTGCTCCCCGATCACCCAGGGTGACAGGGGAGTGGGCTCCAGTGTGTTATTTT 374  
Db 1768 CTGGCCCTGCTCCCCCATCACCCAGGGTGATAGGGAGTGGGCTCCACTGCTGTTATTTCT 1709

QY 375 AGATGATAACTTTGTAAACAAAGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTC 434  
Db 1708 AGATGATAACTTTGTAAACAAAGGCCACAGCCCTAACCTATGACCCCATATGTAAACTACTC 1649

QY 435 CTCCCGCCATACCATACCCAGCCCTTCTCCTACCCTCCCGGTACTTTACCCCCAAACC 494  
Db 1648 CTCCCGCCATACAATCCCCCAACCCTTCTCCTACCCTCCCGTTACTTTCACACCCAAACC 1589

QY 495 TGTCTAGATTTCACATATGATTACTTCCAACCAACAAAGAAACAGCTGTGGCT 554  
Db 1588 TGTCTTGACTCCACTATTGATTACTTCCAACCAATAACAAAGGAATCAGCTTTGGCT 1529

QY 555 GAGACTACAAACTGCTGGAATGTAGACCACGTAGGCCTCGGCACGTGCGTTGCGAAACAG 614  
Db 1528 GAGGCTACAAACCTCTAGAAATGTGGACCACGTAGGCCTCGGCACGTGCGTTGCGAAACAG 1469

QY 615 TATATACGACCGAGGAATACAATATCCGTGTAAACCATGTATGTAACAATTCAGAGAATTTAA 674  
Db 1468 TATATACGACCGAGGACTACAATATCCGTGTAAACCATGTATGTAACAATTCAGAGAATTTAA 1409

QY 675 TTTTAAAGACCCCTTAAACCCCTTAA 702  
Db 1408 TCTTAAAGACCCCTTAAACCCCTTAA 1381

RESULT 12  
US-09-161-092-4/c  
; Sequence 4, Application US/09161092  
; Patent No. 6391314  
; GENERAL INFORMATION:  
; APPLICANT: ALLAN, Gordon  
; APPLICANT: MEEHAN, Brian  
; APPLICANT: CLARK, Edward  
; APPLICANT: HAINES, Deborah  
; APPLICANT: HASSARD, Lori  
; APPLICANT: HARDING, John  
; APPLICANT: CHARREYRE, Catherine E.  
; APPLICANT: CHAPPUIS, Gilles E.  
; TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC  
; TITLE OF INVENTION: REAGENTS  
; FILE REFERENCE: ALLAN  
; CURRENT APPLICATION NUMBER: US/09/161,092  
; CURRENT FILING DATE: 1998-09-25

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/082,558  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 9800873  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-22  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 9803707  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 97/12382  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-03  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 1768  
; TYPE: DNA  
; ORGANISM: Porcine circovirus  
US-09-161-092-4

Query Match 48.4%; Score 340; DB 4; Length 1768;  
Best Local Similarity 92.3%; Pred. No. 4.6e-96;  
Matches 358; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 315 CTGGCCCTGCTCCCCGATCACCCAGGGTGACAGGGGAGTGGGCTCCAGTGTGTTATTTT 374  
Db 1768 CTGGCCCTGCTCCCCCATCACCCAGGGTGATAGGGAGTGGGCTCCACTGCTGTTATTTCT 1709

QY 375 AGATGATAACTTTGTAAACAAAGGCCACAGCCCTTCTCCTACCCTCCCGGTACTTTACCCCCAAACC 494  
Db 1708 AGATGATAACTTTGTAAACAAAGGCCACAGCCCTAACCTATGACCCCATATGTAAACTACTC 1649

QY 435 CTCCCGCCATACCATACCCAGCCCTTCTCCTACCCTCCCGGTACTTTACCCCCAAACC 494  
Db 1648 CTCCCGCCATACAATCCCCCAACCCTTCTCCTACCCTCCCGTTACTTTCACACCCAAACC 1589

QY 495 TGTCTAGATTTCACATATGATTACTTCCAACCAACAAAGAAACAGCTGTGGCT 554  
Db 1588 TGTCTTGACTCCACTATTGATTACTTCCAACCAATAACAAAGGAATCAGCTTTGGCT 1529

QY 555 GAGACTACAAACTGCTGGAATGTAGACCACGTAGGCCTCGGCACGTGCGTTGCGAAACAG 614  
Db 1528 GAGACTACAAACCTCTGGAATGTGGACCACGTAGGCCTCGGCACGTGCGTTGCGAAACAG 1469

QY 615 TATATACGACCGAGGAATACAATATCCGTGTAAACCATGTATGTAACAATTCAGAGAATTTAA 674  
Db 1468 TAAATACGACCGAGGACTACAATATCCGTGTAAACCATGTATGTAACAATTCAGAGAATTTAA 1409

QY 675 TTTTAAAGACCCCTTAAACCCCTTAA 702  
Db 1408 TCTTAAAGACCCCTTAAACCCCTTAA 1381

RESULT 13  
US-09-082-558-6/c  
; Sequence 6, Application US/09082558A  
; Patent No. 6368601  
; GENERAL INFORMATION:  
; APPLICANT: ALLAN, Gordon  
; APPLICANT: MEEHAN, Brian  
; APPLICANT: CLARK, Edward  
; APPLICANT: HAINES, Deborah  
; APPLICANT: HASSARD, Lori  
; APPLICANT: HARDING, John  
; APPLICANT: CHARREYRE, Catherine E.  
; APPLICANT: CHAPPUIS, Gilles E.  
; TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC  
; TITLE OF INVENTION: REAGENTS  
; FILE REFERENCE: ALLAN  
; CURRENT APPLICATION NUMBER: US/09/082,558A  
; CURRENT FILING DATE: 1998-05-21  
; EARLIER APPLICATION NUMBER: FR 9800873  
; EARLIER FILING DATE: 1998-01-22  
; EARLIER APPLICATION NUMBER: FR 9803707  
; EARLIER FILING DATE: 1998-03-20  
; EARLIER APPLICATION NUMBER: FR 97/12382  
; EARLIER FILING DATE: 1997-10-03

; APPLICANT: ELLIS, John A.  
; APPLICANT: KRAKOWKA, George S.  
; APPLICANT: AUDONNET, Jean-Christophe F.  
; TITLE OF INVENTION: PORCINE CIRCOVIRUS AND PARVOVIRUS VACCINE  
; FILE REFERENCE: 454313-2338  
; CURRENT APPLICATION NUMBER: US/09/347,594  
; CURRENT FILING DATE: 1999-07-01  
; EARLIER APPLICATION NUMBER: 98 08777  
; EARLIER FILING DATE: 1998-07-06  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1767  
; TYPE: DNA  
; ORGANISM: Porcine circovirus  
US-09-347-594-2

Query Match 53.9%; Score 378.4; DB 4; Length 1767;  
Best Local Similarity 98.5%; Pred. No. 4.9e-108;  
Matches 382; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY	315	CTGGCCCTGCTCCCGGATCACCCAGGGTGACAGGGGAGTGGGCTCCAGTGGTATT	374
Db	1767	CTGGCCCTGCTCCCGGATCACCCAGGGTGACAGGGGAGTGGGCTCCAGTGGTATT	1708
QY	375	AGATGATAACTTTGTAAAGGCCACAGCCCTCACCTATGACCCCTATGTAATACT	434
Db	1707	AGATGATAACTTTGTAAAGGCCACAGCCCTCACCTATGACCCCTATGTAATACT	1648
QY	435	CTCCCGCCATACCATAACCCAGCCCTTCTCTACCACTCCCGGTACTTTACCCCA	494
Db	1647	CTCCCGCCATACCATAACCCAGCCCTTCTCTACCACTCCCGGTACTTTACCCCA	1588
QY	495	TGTCCTAGATTTCACCTATTGATTACTTCCAACCAACAAAGAAATCAGCTGT	554
Db	1587	TGTCCTAGATTTCACCTATTGATTACTTCCAACCAACAAAGAAATCAGCTGT	1528
QY	555	GAGACTACAAACTGCTGGAAATGTAGACCACGTAGGCCTCGGCACGCGTT	614
Db	1527	GAGACTACAAACTGCTGGAAATGTAGACCACGTAGGCCTCGGCACGCGTT	1468
QY	615	TATATACGACCAAGGAATACAAATATCCGTGTAAACCAATTCAGAGAAT	674
Db	1467	TATATACGACCAAGGAATACAAATATCCGTGTAAACCAATTCAGAGAAT	1408
QY	675	TTTTAAAGACCCCCCACTTAACCCCTTAA 702	
Db	1407	TCTTAAAGACCCCCCACTTAACCCCTTAA 1380	

RESULT 5  
US-09-082-558-2/c  
; Sequence 2, Application US/09082558A  
; Patent No. 6368601  
; GENERAL INFORMATION:  
; APPLICANT: ALLAN, Gordon  
; APPLICANT: MEEHAN, Brian  
; APPLICANT: CLARK, Edward  
; APPLICANT: HAINES, Deborah  
; APPLICANT: HASSARD, Lori  
; APPLICANT: HARDING, John  
; APPLICANT: CHARREYRE, Catherine E.  
; APPLICANT: CHAPPUIS, Gilles E.  
; TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC  
; TITLE OF INVENTION: REAGENTS  
; FILE REFERENCE: ALLAN  
; CURRENT APPLICATION NUMBER: US/09/082,558A  
; CURRENT FILING DATE: 1998-05-21  
; EARLIER APPLICATION NUMBER: FR 9800873  
; EARLIER FILING DATE: 1998-01-22  
; EARLIER APPLICATION NUMBER: FR 9803707  
; EARLIER FILING DATE: 1998-03-20  
; EARLIER APPLICATION NUMBER: FR 97/12382

; EARLIER FILING DATE: 1997-10-03  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1767  
; TYPE: DNA  
; ORGANISM: Porcine circovirus  
US-09-082-558-2

Query Match 53.9%; Score 378.4; DB 4; Length 1767;  
Best Local Similarity 98.5%; Pred. No. 4.9e-108;  
Matches 382; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY	315	CTGGCCCTGCTCCCGGATCACCCAGGGTGACAGGGGAGTGGGCTCCAGTGGTATT	374
Db	1767	CTGGCCCTGCTCCCGGATCACCCAGGGTGACAGGGGAGTGGGCTCCAGTGGTATT	1708
QY	375	AGATGATAACTTTGTAAAGGCCACAGCCCTCACCTATGACCCCTATGTAATACT	434
Db	1707	AGATGATAACTTTGTAAAGGCCACAGCCCTCACCTATGACCCCTATGTAATACT	1648
QY	435	CTCCCGCCATACCATAACCCAGCCCTTCTCTACCACTCCCGGTACTTTACCCCA	494
Db	1647	CTCCCGCCATACCATAACCCAGCCCTTCTCTACCACTCCCGGTACTTTACCCCA	1588
QY	495	TGTCCTAGATTTCACCTATTGATTACTTCCAACCAACAAAGAAATCAGCTGT	554
Db	1587	TGTCCTAGATTTCACCTATTGATTACTTCCAACCAACAAAGAAATCAGCTGT	1528
QY	555	GAGACTACAAACTGCTGGAAATGTAGACCACGTAGGCCTCGGCACGCGTT	614
Db	1527	GAGACTACAAACTGCTGGAAATGTAGACCACGTAGGCCTCGGCACGCGTT	1468
QY	615	TATATACGACCAAGGAATACAAATATCCGTGTAAACCAATTCAGAGAAT	674
Db	1467	TATATACGACCAAGGAATACAAATATCCGTGTAAACCAATTCAGAGAAT	1408
QY	675	TTTTAAAGACCCCCCACTTAACCCCTTAA 702	
Db	1407	TCTTAAAGACCCCCCACTTAACCCCTTAA 1380	

RESULT 6  
US-09-161-092-2/c  
; Sequence 2, Application US/09161092  
; Patent No. 6391314  
; GENERAL INFORMATION:  
; APPLICANT: ALLAN, Gordon  
; APPLICANT: MEEHAN, Brian  
; APPLICANT: CLARK, Edward  
; APPLICANT: HAINES, Deborah  
; APPLICANT: HASSARD, Lori  
; APPLICANT: HARDING, John  
; APPLICANT: CHARREYRE, Catherine E.  
; APPLICANT: CHAPPUIS, Gilles E.  
; TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC  
; TITLE OF INVENTION: REAGENTS  
; FILE REFERENCE: ALLAN  
; CURRENT APPLICATION NUMBER: US/09/161,092  
; CURRENT FILING DATE: 1998-09-25  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/082,558  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 9800873  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-22  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 9803707  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 97/12382  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1767  
; TYPE: DNA





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2003, 11:03:33 ; Search time 55 Seconds  
(without alignments)  
3914.311 Million cell updates/sec

Title: US-09-514-245B-25  
Perfect score: 702  
Sequence: 1 atgacgtatccaaggaggcg.....acccccacttaacccttaa 702

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters.: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	381.6	54.4	1767	4 US-09-347-594-1	Sequence 1, Appli
C 2	381.6	54.4	1767	4 US-09-082-558-1	Sequence 1, Appli
C 3	381.6	54.4	1767	4 US-09-161-092-1	Sequence 1, Appli
C 4	378.4	53.9	1767	4 US-09-347-594-2	Sequence 2, Appli
C 5	378.4	53.9	1767	4 US-09-082-558-2	Sequence 2, Appli
C 6	378.4	53.9	1767	4 US-09-161-092-2	Sequence 3, Appli
C 7	340	48.4	1768	4 US-09-347-594-3	Sequence 3, Appli
C 8	340	48.4	1768	4 US-09-347-594-4	Sequence 3, Appli
C 9	340	48.4	1768	4 US-09-082-558-3	Sequence 3, Appli
C 10	340	48.4	1768	4 US-09-082-558-4	Sequence 4, Appli
C 11	340	48.4	1768	4 US-09-161-092-3	Sequence 3, Appli
C 12	340	48.4	1768	4 US-09-161-092-4	Sequence 4, Appli
C 13	339	48.3	1768	4 US-09-082-558-6	Sequence 6, Appli
C 14	339	48.3	1768	4 US-09-161-092-6	Sequence 6, Appli
C 15	307.8	43.8	699	4 US-09-267-177-24	Sequence 24, Appli
C 16	307.8	43.8	1727	4 US-09-267-177-2	Sequence 2, Appli
C 17	307.8	43.8	1759	4 US-09-267-177-38	Sequence 38, Appli
C 18	307.8	43.8	1759	4 US-09-267-177-40	Sequence 40, Appli
C 19	303.2	43.2	687	4 US-09-267-177-25	Sequence 25, Appli
C 20	299	42.6	1674	4 US-09-267-177-1	Sequence 1, Appli
C 21	199.4	28.4	1759	4 US-09-347-594-5	Sequence 5, Appli
C 22	199.4	28.4	1759	4 US-09-082-558-5	Sequence 5, Appli
C 23	199.4	28.4	1759	4 US-09-161-092-5	Sequence 5, Appli
C 24	172.2	24.5	285	4 US-09-267-177-22	Sequence 22, Appli
C 25	44.6	6.4	4403765	4 US-09-103-840A-2	Sequence 2, Appli
C 26	44.6	6.4	4411529	4 US-09-103-840A-1	Sequence 1, Appli
C 27	41.8	6.0	322	4 US-09-117-121-41	Sequence 41, Appli

28	41.8	6.0	322	4 US-09-344-529-7	Sequence 7, Appli
29	41.8	6.0	9997	1 US-08-246-982A-15	Sequence 15, Appli
30	41.8	6.0	9997	1 US-08-453-265-15	Sequence 15, Appli
31	41.8	6.0	10103	2 US-08-457-273B-7	Sequence 7, Appli
32	41.8	6.0	10348	2 US-08-457-273B-41	Sequence 41, Appli
33	41.8	6.0	10348	3 US-08-556-419-13	Sequence 13, Appli
34	41.8	6.0	10348	4 US-09-041-886-14	Sequence 14, Appli
35	41.8	6.0	10366	1 US-08-246-982A-5	Sequence 5, Appli
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C 38	40	5.7	6530	3 US-08-458-240-1	Sequence 1, Appli
C 39	40	5.7	6530	5 PCT-US93-03993-1	Sequence 1, Appli
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C 41	39.4	5.6	1028	4 US-08-118-200-1	Sequence 1, Appli
C 42	39.4	5.6	1028	4 US-08-458-745-1	Sequence 1, Appli
C 43	39.4	5.6	3572	4 US-09-575-574-3	Sequence 3, Appli
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45	39.4	5.6	4411529	4 US-09-103-840A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-09-347-594-1/c  
; Sequence 1, Application US/09347594  
; Patent No. 6217883  
; GENERAL INFORMATION:  
; APPLICANT: ALLAN, Gordon M.  
; APPLICANT: MEEHAN, Brian M.  
; APPLICANT: ELLIS, John A.  
; APPLICANT: KRAKOWKA, George S.  
; APPLICANT: AUDONNET, Jean-Christophe F.  
; TITLE OF INVENTION: PORCINE CIRCOVIRUS AND PARVOVIRUS VACCINE  
; FILE REFERENCE: 454313-2338  
; CURRENT APPLICATION NUMBER: US/09/347,594  
; CURRENT FILING DATE: 1999-07-01  
; EARLIER APPLICATION NUMBER: 98 08777  
; EARLIER FILING DATE: 1998-07-06  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1767  
; TYPE: DNA  
; ORGANISM: Porcine circovirus  
US-09-347-594-1

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Best Local Similarity	99.0%	Pred. NO. 5e-109;		
Matches	384;	Conservative	0;	Mismatches 4;
				Indels 0;
				Gaps 0;
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Db	1767	CTGGCCCTGCTCCCGGATCACCAGGGTGACAGGGGAGTGGGCTCCAGTGGCTGTTATTTCT	1708	
QY	375	AGATGATAACTTTGTAAACAAAGGCCACAGCCCTCACCTATGACCCCTATGTAACACTACTC	434	
Db	1707	AGATGATAACTTTGTAAACAAAGGCCACAGCCCTCACCTATGACCCCTATGTAACACTACTC	1648	
QY	435	CTCCCGGCATACCATAACCCAGCCCTTCTCTCTACCACCTCCCGGTACTTTACCCCAAAACC	494	
Db	1647	CTCCCGGCATACCATAACCCAGCCCTTCTCTCTACCACCTCCCGGTACTTTACCCCAAAACC	1588	
QY	495	TGTCCTAGATTTCACCTATTGATTACTTCCACAAACAAACAAAGAACCCAGCTGTGGCT	554	
Db	1587	TGTCCTAGATTTCACCTATTGATTACTTCCACAAACAAACAAAGAACCCAGCTGTGGCT	1528	
QY	555	GAGACTACAAACTGCTGGAAATGTAGACCACGTTAGGCCTCGGCACCTGCCGTTTCGAAAACAG	614	
Db	1527	GAGACTACAAACTGCTGGAAATGTAGACCACGTTAGGCCTCGGCACCTGCCGTTTCGAAAACAG	1468	
QY	615	TATATACGACGAGGAATACAATATCCGTGTAAACCATGTATGTACAAATTCAGAGAAATTA	674	





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/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
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Best Local Similarity 58.5%; Pred. No. 0.12;
Matches 79; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 32 GAAGACACCGCCCGCAGCCATCTTGGCCAGATCTCCGCCGCCGCCCTGGCTCGTCC 91
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QY 92 ACCCCGCCACCGTTACCGCTGGAGAGGAAAATGGCATCTTCAACACCGCGCTCTCCC 151
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QY 152 GCACCTTCGGATATA 166
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Db 440 ACCTCCTCCGGAATA 426
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RESULT 2
CNS00CNG
LOCUS      939 bp      DNA      linear      GSS 04-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR26H16 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION  AL059400
VERSION     AL059400.1 GI:4946964
KEYWORDS   GSS.
SOURCE     Drosophila melanogaster.
            Drosophila melanogaster.
ORGANISM   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1 (bases 1 to 939)
            Genoscope.
            Direct Submission
            Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT    Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mamoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
            p1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Best Local Similarity 18.1%; Pred. No. 0.23;
Matches 56; Conservative 122; Mismatches 131; Indels 0; Gaps 0;

QY 391 ACAAAGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTCCTCCCGCCATACCATA 450
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Db 274 MMHAWMCCTTCCCTCCCYCMCYTCCCCCCCCCAYYYMCCCMCCCTTCTYCCCATCCMMC 333

QY 451 ACCGAGCCCTTCTCTACCACTCCCGGTACTTTACCCCAACCTGTCTAGATTTCAC 510
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Db 334 CCCTCTCCCGCCMCCYATCCCTCMMMYHTTYMMCCCCCCCCCMCHMTCCMMMMMM 393

QY 511 ATTGATTACTTCCAAACCAACAAAGAAAGAACAGCTGTGGCTGAGACTACAAACTGCT 570
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Db 394 MMMMMMMMTMHMMMMMMMTMMHMMMTTMMHMMMTTMMHMMMTTMMHMMMTTMMTMM 453

QY 571 GGAATGTAGACCACGTAGCCCTCGGCACCTCGCTTCGAAACAGTATATACGACCAGAA 630
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 454 MMMMMMMMMMTMMHMMMMMTTMMHMMMTTMMHMMMTTMMHMMMTTMMHMMMTTMMH 513

QY 631 TACAATATCCGTCTAACCATGTATGTACATTCAGAGAAATTTAAAGACCCCCCA 690
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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QY 691 CTTAACCCCT 699
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Db 574 CGTCTCTCT 582
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RESULT 3
BI629442/c
LOCUS      638 bp      mRNA      linear      EST 10-SEP-2001
DEFINITION RH58310.5prime RH Drosophila melanogaster normalized Head pFlc-1
            Drosophila melanogaster cDNA clone RH58310 5 similar to CG17108:
            FBan0017108 GO:[ ] located on: 2L 32A1-32A1;; 08/23/2001, mRNA
            sequence.
ACCESSION  BI629442
VERSION     BI629442.1 GI:15531652
KEYWORDS   EST.
SOURCE     fruit fly.
ORGANISM   Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1 (bases 1 to 638)
            Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson
            ,J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George
            ,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S.,
            Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S.,
            Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin
            ,G.M.
            BDGP/HMI RH Drosophila EST Project
            Unpublished (2001)
            Contact: Stapleton, M.
            BDGP
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TITLE      Lawrence Berkeley National Lab
JOURNAL     One Cyclotron Rd, Berkeley, CA 94720, USA
COMMENT     Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            hit genomic AE003629; arm:2L [10413221,10674011]
            estimated-cyto:31E5-32A5: 08/23/2001
            Plate: RH.583 row: A column: 10
            High quality sequence stop: 511.
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                     /clone_lib="RH Drosophila melanogaster normalized Head
                     pFlc-1"
                     /sex="male and female"
                     /dev_stage="Adult"
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2003, 10:32:44 ; Search time 1499 Seconds  
(without alignments)  
7584.544 Million cell updates/sec

Title: US-09-514-245B-25  
Perfect score: 702  
Sequence: 1 atgacgtatccaaggaggcg.....acccccacttaacccttaa 702

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3:	em_estin:*		
4:	em_estmu:*		
5:	em_estov:*		
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7:	em_estro:*		
8:	em_htc:*		
9:	gb_est1:*		
10:	gb_est2:*		
11:	gb_htc:*		
12:	gb_est3:*		
13:	gb_est4:*		
14:	gb_est5:*		
15:	em_estfun:*		
16:	em_estom:*		
17:	gb_gss:*		
18:	em_gss_hum:*		
19:	em_gss_inv:*		
20:	em_gss_pln:*		
21:	em_gss_vrt:*		
22:	em_gss_fun:*		
23:	em_gss_mam:*		
24:	em_gss_mus:*		
25:	em_gss_other:*		
26:	em_gss_pro:*		
27:	em_gss_rod:*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
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C 4	44	6.3	445	9 AI292664	AI292664 GH15617.5
C 5	44	6.3	484	9 AI108264	AI108264 GH07058.5
C 6	44	6.3	493	9 AI405757	AI405757 GH25879.5

C 7	44	6.3	497	9 AI238309	AI238309 GH14332.5
C 8	44	6.3	532	9 AI134557	AI134557 GH12051.5
C 9	44	6.3	557	9 AI404106	AI404106 GH23705.5
C 10	44	6.3	557	9 AI406114	AI406114 GH26313.5
C 11	44	6.3	558	9 AI238565	AI238565 GH14632.5
C 12	44	6.3	561	9 AI404901	AI404901 GH24758.5
C 13	44	6.3	561	9 AI406248	AI406248 GH26478.5
C 14	44	6.3	575	9 AI403207	AI403207 GH22602.5
C 15	44	6.3	593	9 AI516823	AI516823 GH27392.5
C 16	44	6.3	597	13 BI627948	BI627948 RH69450.5
C 17	44	6.3	613	9 AI237965	AI237965 GH13172.5
18	44	6.3	653	14 BQ161715	BQ161715 WHE0472_A
C 19	43.8	6.2	554	9 AI293059	AI293059 GH16139.5
C 20	43.8	6.2	870	12 BG445569	BG445569 GA_Ea002
C 21	43.4	6.2	479	9 AI402428	AI402428 GH21648.5
C 22	43.2	6.2	521	9 AA530753	AA530753 vJ44e07.r
C 23	43.2	6.2	555	9 AI296628	AI296628 LP10591.5
C 24	43.2	6.2	574	13 BI619435	BI619435 RH50469.5
C 25	43.2	6.2	575	13 BI619848	BI619848 RH50971.5
26	43.2	6.2	591	9 AI857154	AI857154 603007B08
C 27	43.2	6.2	597	14 BQ704127	BQ704127 946110E10
28	43.2	6.2	674	17 BH879805	BH879805 ht48h11.g
C 29	43.2	6.2	835	11 AK020691	AK020691 Mus muscu
C 30	43	6.1	452	9 AA589477	AA589477 v147h12.s
C 31	43	6.1	514	9 AA798859	AA798859 vv94a07.r
C 32	43	6.1	617	12 BG591496	BG591496 EST499338
C 33	43	6.1	636	9 AA698799	AA698799 HL05714.5
34	43	6.1	650	12 BG599848	BG599848 EST504743
C 35	43	6.1	-706	13 BM110666	BM110666 EST558202
36	43	6.1	710	12 BF253141	BF253141 EST445636
C 37	42.8	6.1	1064	17 CNS01N6W	AL151849 Anopheles
38	42.6	6.1	449	10 AW615354	AW615354 hh74b04.x
39	42.6	6.1	494	9 AI141028	AI141028 oy68h12.x
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C 41	42.6	6.1	574	13 BI799844	BI799844 H142B04 E
C 42	42.6	6.1	575	14 C99980	C99980 C99980 Oryz
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ALIGNMENTS

RESULT 1	AI514058/c	AI514058	561 bp	mrna	linear	EST 19-APR-2001
LOCUS	GH27112.5prime GH Drosophila melanogaster head	GH27112.5prime	5prime	GH Drosophila	melanogaster head	pOT2 Drosophila
DEFINITION	melanogaster cDNA clone	GH27112	5prime	mrna	sequence.	
ACCESSION	AI514058	AI514058				
VERSION	AI514058.1	GI:4418120				
KEYWORDS	EST					
SOURCE	fruit fly.					
ORGANISM	Drosophila melanogaster					
REFERENCE	1 (bases 1 to 561)					
AUTHORS	Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.					
TITLE	BDGP/HMI Drosophila EST Project					
JOURNAL	Unpublished (2001)					
COMMENT	Contact: Stapleton, M. BDGP					
	Lawrence Berkeley National Lab					
	One Cyclotron Rd, Berkeley, CA 94720, USA					
	Fax: 510 486 6798					
	Email: <a href="http://www.fruitfly.org/EST">http://www.fruitfly.org/EST</a> , <a href="mailto:est@fruitfly.berkeley.edu">est@fruitfly.berkeley.edu</a>					
	Plate: 271 row: A column: 12					
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ACCESSION AI405757
VERSION AI405757.1 GI:4248844
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 493)
AUTHORS Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
BDGP/HMI Drosophila EST Project
Unpublished (2001)
JOURNAL
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 258 row: G column: 7
High quality sequence stop: 492.
Location/Qualifiers
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/clone="GH25879"
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/sex="male and female"
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/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
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ORIGIN
Query Match 6.3%; Score 44; DB 9; Length 493;
Best Local Similarity 58.3%; Pred. No. 0.29;
Matches 77; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 35 GACACCGCCCGCAGCATCTTGGCCAGATCCTCCGCCGCGCCCTGGCTCGTCCACC 94
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Db 332 GATTCCACCGCTCCACCAGATGGCCACCTCCGCCGCGGATTCGCCACCAATCCAGG 273
QY 95 CCCGCCACCGTTACCGCTGGAGAGGAAATGGCATCTTCAACACCGCGCTCTCCCGCA 154
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Db 272 GCGGCCACCGATTCCGCTACCTCCACCAGATGGCCACCTCCACCGCGCGATTCGGCCACC 213
QY 155 CCTTCGGATATA 166
Db 212 TCCTCCGGAATA 201
RESULT 7
AI238309/c
LOCUS 497 bp mRNA linear EST 19-APR-2001
DEFINITION GH14332.5prime GH Drosophila melanogaster head pOT2 Drosophila
melanogaster cDNA clone GH14332 5prime, mRNA sequence.
ACCESSION AI238309.1 GI:3833167
VERSION
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 497)
AUTHORS Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
BDGP/HMI Drosophila EST Project
Unpublished (2001)
JOURNAL
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 120 row: E column: 3
High quality sequence stop: 403.
Location/Qualifiers
1..532
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GH12051"
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/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
ACCESSION AI405757
VERSION AI405757.1 GI:3627115
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 532)
AUTHORS Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
BDGP/HMI Drosophila EST Project
Unpublished (2001)
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 120 row: E column: 3
High quality sequence stop: 403.
Location/Qualifiers
1..532
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GH12051"
/clone_lib="GH Drosophila melanogaster head pOT2"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
ACCESSION AI134557
VERSION AI134557.1 GI:3627115
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 532)
AUTHORS Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
BDGP/HMI Drosophila EST Project
Unpublished (2001)
JOURNAL
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 120 row: E column: 3
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/clone_lib="GH Drosophila melanogaster head pOT2"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
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Best Local Similarity 58.3%; Pred. No. 0.29;
Matches 77; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 35 GACACCGCCCGCAGCATCTTGGCCAGATCCTCCGCCGCGCCCTGGCTCGTCCACC 94
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Db 181 GATTCCACCGCTCCACCAGATGGCCACCTCCGCCGCGGATTCGCCACCAATCCAGG 122
QY 95 CCCGCCACCGTTACCGCTGGAGAGGAAATGGCATCTTCAACACCGCGCTCTCCCGCA 154
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Db 121 GCGGCCACCGATTCCGCTACCTCCACCAGATGGCCACCTCCACCGCGCGATTCGGCCACC 62
QY 155 CCTTCGGATATA 166
Db 61 TCCTCCGGAATA 50
RESULT 8
AI134557/c
LOCUS 532 bp mRNA linear EST 19-APR-2001
DEFINITION GH12051.5prime GH Drosophila melanogaster head pOT2 Drosophila
melanogaster cDNA clone GH12051 5prime, mRNA sequence.
ACCESSION AI134557.
VERSION AI134557.1 GI:3627115
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 532)
AUTHORS Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
BDGP/HMI Drosophila EST Project
Unpublished (2001)
JOURNAL
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 120 row: E column: 3
High quality sequence stop: 403.
Location/Qualifiers
1..532
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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/clone_lib="GH Drosophila melanogaster head pOT2"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
BASE COUNT 80 a 96 c 222 g 99 t
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Query Match 6.3%; Score 44; DB 9; Length 497;
Best Local Similarity 58.3%; Pred. No. 0.29;
Matches 77; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 35 GACACCGCCCGCAGCATCTTGGCCAGATCCTCCGCCGCGCCCTGGCTCGTCCACC 94
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Db 121 GCGGCCACCGATTCCGCTACCTCCACCAGATGGCCACCTCCACCGCGCGATTCGGCCACC 62
QY 155 CCTTCGGATATA 166
Db 61 TCCTCCGGAATA 50
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Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 143 row: C column: 8
High quality sequence stop: 457.
Location/Qualifiers
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/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
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pOT2. Plasmid cDNA library."
BASE COUNT 80 a 96 c 222 g 99 t
ORIGIN
Query Match 6.3%; Score 44; DB 9; Length 497;
Best Local Similarity 58.3%; Pred. No. 0.29;
Matches 77; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 35 GACACCGCCCGCAGCATCTTGGCCAGATCCTCCGCCGCGCCCTGGCTCGTCCACC 94
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Db 181 GATTCCACCGCTCCACCAGATGGCCACCTCCGCCGCGGATTCGCCACCAATCCAGG 122
QY 95 CCCGCCACCGTTACCGCTGGAGAGGAAATGGCATCTTCAACACCGCGCTCTCCCGCA 154
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Db 121 GCGGCCACCGATTCCGCTACCTCCACCAGATGGCCACCTCCACCGCGCGATTCGGCCACC 62
QY 155 CCTTCGGATATA 166
Db 61 TCCTCCGGAATA 50
RESULT 8
AI134557/c
LOCUS 532 bp mRNA linear EST 19-APR-2001
DEFINITION GH12051.5prime GH Drosophila melanogaster head pOT2 Drosophila
melanogaster cDNA clone GH12051 5prime, mRNA sequence.
ACCESSION AI134557.
VERSION AI134557.1 GI:3627115
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 532)
AUTHORS Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
BDGP/HMI Drosophila EST Project
Unpublished (2001)
JOURNAL
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 120 row: E column: 3
High quality sequence stop: 403.
Location/Qualifiers
1..532
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GH12051"
/clone_lib="GH Drosophila melanogaster head pOT2"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
BASE COUNT 80 a 96 c 222 g 99 t
ORIGIN
Query Match 6.3%; Score 44; DB 9; Length 497;
Best Local Similarity 58.3%; Pred. No. 0.29;
Matches 77; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 35 GACACCGCCCGCAGCATCTTGGCCAGATCCTCCGCCGCGCCCTGGCTCGTCCACC 94
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Db 181 GATTCCACCGCTCCACCAGATGGCCACCTCCGCCGCGGATTCGCCACCAATCCAGG 122
QY 95 CCCGCCACCGTTACCGCTGGAGAGGAAATGGCATCTTCAACACCGCGCTCTCCCGCA 154
||||| || || || || || || || || || || || || || || || || || || || ||
Db 121 GCGGCCACCGATTCCGCTACCTCCACCAGATGGCCACCTCCACCGCGCGATTCGGCCACC 62
QY 155 CCTTCGGATATA 166
Db 61 TCCTCCGGAATA 50
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/lab_host="DH5-alpha Tona"
/note="Organ: head; Vector: pFlcl; Site_1: XhoI; Site_2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."
BASE COUNT      87 a   127 c   269 g   153 t       2 others
ORIGIN

Query Match      6.3%; Score 44.2; DB 13; Length 638;
Best Local Similarity 57.2%; Pred. No. 0.27;
Matches 79; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 29 GAAGAAGACACCGCCCGCAGCCATCTTGGCCAGATCCTCCGCCCGCCCTGGCTCG 88
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Db 581 GCNGCCGATTCCACCGCCTCCACCAGAATGGCCACCTCCGCCCGCGATTCCGCCACCAA 522
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QY 89 TCCACCCCGCCCGCTTACCGCTGGAGAGGAAATGGCATCTTCAACACCCGCTCT 148
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Db 521 TCCAGGGCGCGCCCGGATTCGGCTACCTCCACCAGAATGGCCACCTCCACCGCGGATTCC 462
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QY 149 CCCGCACCTTCGGATATA 166
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Db 461 GCCACCTCCTCCGGAATA 444

RESULT 4
AI292664/c
LOCUS
DEFINITION
  GH15617.5prime GH Drosophila melanogaster head pOT2 Drosophila
  melanogaster cDNA clone GH15617 5prime, mRNA sequence.
ACCESSION
  AI292664
VERSION
  AI292664.1 GI:3942071
KEYWORDS
  EST.
SOURCE
  fruit fly.
ORGANISM
  Drosophila melanogaster
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
  Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
  1 (bases 1 to 445)
AUTHORS
  Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
  Lewis,S. and Rubin,G.M.
  BDGP/HMI Drosophila EST Project
  Unpublished (2001)
  Contact: Stapleton, M.
  BDGP
  Lawrence Berkeley National Lab
  One Cyclotron Rd, Berkeley, CA 94720, USA
  Fax: 510 486 6798
  Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
  Plate: 156 row: B column: 5
  High quality sequence stop: 293.
  Location/Qualifiers
    1..445
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    /db_xref="taxon:7227"
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    /sex="male and female"
    /dev_stage="adult"
    /lab_host="DH5 - alpha"
    /note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
    XhoI; Sized fractionated cDNAs were directly ligated into
    pOT2. Plasmid cDNA library."
    pOT2. Plasmid cDNA library.
BASE COUNT      64 a   87 c   193 g   101 t
ORIGIN

Query Match      6.3%; Score 44; DB 9; Length 445;
Best Local Similarity 58.3%; Pred. No. 0.28;
Matches 77; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 35 GACACCGCCCGCAGCCATCTTGGCCAGATCCTCCGCCCGCCCTGGCTCGTCCACC 94
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Db 389 GATTCCACCGCTCCACCAGAATGGCCACCTCCGCCCGCGATTCCGCCACCAATCCAGG 330
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QY 95 CCCGCCACCGTTACCGCTGGAGAGGAAATGGCATCTTCAACACCCCGCTCTCCCGCA 154
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Db 329 GCCGCCACCGATTCCGCTACCTCCACCAGAATGGCCACCTCCACCGCGGATTCCGCCACC 270
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QY 155 CCTTCGGATATA 166
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Db 269 TCCTCCGGAATA 258

RESULT 5
AI108264/c
LOCUS
DEFINITION
  GH07058.5prime GH Drosophila melanogaster head pOT2 Drosophila
  melanogaster cDNA clone GH07058 5prime, mRNA sequence.
ACCESSION
  AI108264
VERSION
  AI108264.1 GI:3476543
KEYWORDS
  EST.
SOURCE
  fruit fly.
ORGANISM
  Drosophila melanogaster
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
  Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
  1 (bases 1 to 484)
AUTHORS
  Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
  Lewis,S. and Rubin,G.M.
  BDGP/HMI Drosophila EST Project
  Unpublished (2001)
  Contact: Stapleton, M.
  BDGP
  Lawrence Berkeley National Lab
  One Cyclotron Rd, Berkeley, CA 94720, USA
  Fax: 510 486 6798
  Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
  Plate: 70 row: E column: 10
  High quality sequence stop: 404.
  Location/Qualifiers
    1..484
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    /db_xref="taxon:7227"
    /clone="GH07058"
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    XhoI; Sized fractionated cDNAs were directly ligated into
    pOT2. Plasmid cDNA library."
    pOT2. Plasmid cDNA library.
BASE COUNT      69 a   88 c   212 g   115 t
ORIGIN

Query Match      6.3%; Score 44; DB 9; Length 484;
Best Local Similarity 58.3%; Pred. No. 0.29;
Matches 77; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 35 GACACCGCCCGCAGCCATCTTGGCCAGATCCTCCGCCCGCCCTGGCTCGTCCACC 94
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Db 401 GATTCCACCGCTCCACCAGAATGGCCACCTCCGCCCGCGATTCCGCCACCAATCCAGG 342
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QY 95 CCCGCCACCGTTACCGCTGGAGAGGAAATGGCATCTTCAACACCCCGCTCTCCCGCA 154
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Db 341 GCCGCCACCGATTCCGCTACCTCCACCAGAATGGCCACCTCCACCGCGGATTCCGCCACC 282
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QY 155 CCTTCGGATATA 166
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Db 281 TCCTCCGGAATA 270

RESULT 6
AI405757/c
LOCUS
DEFINITION
  GH25879.5prime GH Drosophila melanogaster head pOT2 Drosophila
  melanogaster cDNA clone GH25879 5prime, mRNA sequence.
ACCESSION
  AI405757
VERSION
  AI405757.1 GI:108264
KEYWORDS
  EST.
SOURCE
  fruit fly.
ORGANISM
  Drosophila melanogaster
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
  Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
  1 (bases 1 to 493)
AUTHORS
  Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
  Lewis,S. and Rubin,G.M.
  BDGP/HMI Drosophila EST Project
  Unpublished (2001)
  Contact: Stapleton, M.
  BDGP
  Lawrence Berkeley National Lab
  One Cyclotron Rd, Berkeley, CA 94720, USA
  Fax: 510 486 6798
  Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
  Plate: 70 row: E column: 10
  High quality sequence stop: 404.
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    /dev_stage="adult"
    /lab_host="DH5 - alpha"
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    XhoI; Sized fractionated cDNAs were directly ligated into
    pOT2. Plasmid cDNA library."
    pOT2. Plasmid cDNA library.
BASE COUNT      69 a   88 c   212 g   115 t
ORIGIN

Query Match      6.3%; Score 44; DB 9; Length 484;
Best Local Similarity 58.3%; Pred. No. 0.29;
Matches 77; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
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QY 241 CCCCCAGGAGGGGTCAAAACCCCGCTCTGTGCCCTTTGAACTACTACAGAATAAGAAAG 300  
Db 1495 CCCCCGAGGGGGACCAACAAAATCTCTATACCCCTTGAATACTACAGAATAAGAAAG 1436  
QY 301 GTTAAGGTTGAATTTCTGGCCCTGCTCCCGATCACCCAGGTTGACAGGGGAGTGGGCTCC 360  
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QY 361 AGTGCTGTTATTTAGATGATAAATTTGTAAACAAAGGCCACAGCCCTCACCTATGACCCC 420  
Db 1375 ACTGCTGTTATTTAGATGATAAATTTGTAAACAAAGGCCACAGCCCTAACCTATGACCCA 1316  
QY 421 TATGTAACACTACTCCTCCCGCCATACCATAAACCCAGCCCTTCTCCTACCACCTCCCGGTAC 480  
Db 1315 TATGTAACACTACTCCTCCCGCCATACCAATCCCCCAACCCCTTCTCCTACCACCTCCCGTTAC 1256  
QY 481 TTTACCCCCAAACCTGTCTAGATTTTCACTATTGATTACTTCCAAACCAACAAACAAAGA 540  
Db 1255 TTCACACCCAAACCTGTTCTTGACTCCACTATTGATTACTTCCAAACCAACAAACAAAG 1196  
QY 541 AACCAGCTGTGGCTGAGACTACAAACTGCTGGAAATGTAGACCACGTAGGCCCTCGGCAC 600  
Db 1195 AATCAGCTTTGGCTGAGGCTACAAACCTCTGGAAATGTGACCAACGTAGGCCCTCGGCAC 1136  
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RESULT 2  
US-09-935-428A-1/c  
; Sequence 1, Application US/09935428A  
; Patent No. US20020106639A1  
; GENERAL INFORMATION:  
; APPLICANT: WANG, LI  
; APPLICANT: BABIUK, LORNE A.  
; APPLICANT: POTTER, ANDREW A.  
; APPLICANT: WILLSON, PHILIP  
; TITLE OF INVENTION: POSTWEANING MULTISYSTEM WASTING SYNDROME VIRUS FROM  
; TITLE OF INVENTION: PIGS  
; FILE REFERENCE: 9000-0040  
; CURRENT APPLICATION NUMBER: US/09/935,428A  
; CURRENT FILING DATE: 2001-08-20  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/209,961  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,233  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-11  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,750  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-16  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1768  
; TYPE: DNA  
; ORGANISM: Porcine Circovirus Type II  
US-09-935-428A-1

Query Match 88.4%; Score 620.4; DB 10; Length 1768;  
Best Local Similarity 92.7%; Pred. No. 2.3e-195;  
Matches 651; Conservative 0; Mismatches 51; Indels 0; Gaps 0;  
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Db 1735 ATGACGTATCCAAAGGAGCGGTTACCGCAGAAGAAGACACCGCCCCCGCAGCCATCTTGGC 1676  
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Db 1495 CCCCCGAGGGGGACCAACAAAATCTCTATACCCCTTGAATACTACAGAATAAGAAAG 1436  
QY 301 GTTAAGGTTGAATTTCTGGCCCTGCTCCCGATCACCCAGGTTGACAGGGGAGTGGGCTCC 360  
Db 1435 GTTAAGGTTGAATTTCTGGCCCTGCTCCCGATCACCCAGGTTGATAGGGGAGTGGGCTCC 1376  
QY 361 AGTGCTGTTATTTAGATGATAAATTTGTAAACAAAGGCCACAGCCCTCACCTATGACCCC 420  
Db 1375 ACTGCTGTTATTTAGATGATAAATTTGTAAACAAAGGCCACAGCCCTAACCTATGACCCA 1316  
QY 421 TATGTAACACTACTCCTCCCGCCATACCATAAACCCAGCCCTTCTCCTACCACCTCCCGGTAC 480  
Db 1315 TATGTAACACTACTCCTCCCGCCATACCAATCCCCCAACCCCTTCTCCTACCACCTCCCGTTAC 1256  
QY 481 TTTACCCCCAAACCTGTCTAGATTTTCACTATTGATTACTTCCAAACCAACAAACAAAGA 540  
Db 1255 TTCACACCCAAACCTGTTCTTGACTCCACTATTGATTACTTCCAAACCAACAAACAAAG 1196  
QY 541 AACCAGCTGTGGCTGAGACTACAAACTGCTGGAAATGTAGACCACGTAGGCCCTCGGCAC 600  
Db 1195 AATCAGCTTTGGCTGAGGCTACAAACCTCTGGAAATGTGACCAACGTAGGCCCTCGGCAC 1136  
QY 601 GCGTTCGAAAACAGTATATACGACCAGGAAATACAATATCCGTGTAACCATGTATGTACAA 660  
Db 1135 GCGTTCGAAAACAGTAAATACGACCAGGACTACAATATCCGTGTAACCATGTATGTACAA 1076  
QY 661 TTCAGAGAATTTAATTTTAAAGACCCCCCCTTAAACCCCTTAA 702  
Db 1075 TTCAGAGAATTTAATCTTAAAGACCCCCCCTTAAACCCCTTAA 1034

RESULT 3  
US-09-935-428A-24/c  
; Sequence 24, Application US/09935428A  
; Patent No. US20020106639A1  
; GENERAL INFORMATION:  
; APPLICANT: WANG, LI  
; APPLICANT: BABIUK, LORNE A.  
; APPLICANT: POTTER, ANDREW A.  
; APPLICANT: WILLSON, PHILIP  
; TITLE OF INVENTION: POSTWEANING MULTISYSTEM WASTING SYNDROME VIRUS FROM  
; TITLE OF INVENTION: PIGS  
; FILE REFERENCE: 9000-0040  
; CURRENT APPLICATION NUMBER: US/09/935,428A  
; CURRENT FILING DATE: 2001-08-20  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/209,961  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,233  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-11  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,750  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-16  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 1343  
; TYPE: DNA  
; ORGANISM: Porcine Circovirus Type II

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2003, 11:41:54 ; Search time 164 Seconds  
(without alignments)  
5521.565 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 810007 seqs, 644969091 residues

Total number of hits satisfying chosen parameters: 1620014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*

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13:	/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %		DB ID	Description
	Score	Match		
C 1	623.6	88.8	1768 10 US-09-935-428A-11	Sequence 11, Appl
C 2	620.4	88.4	1768 10 US-09-935-428A-1	Sequence 1, Appli
C 3	618.8	88.1	1343 10 US-09-935-428A-24	Sequence 24, Appl
C 4	618.8	88.1	1768 9 US-10-112-540-1	Sequence 1, Appli
C 5	381.6	54.4	1767 10 US-09-784-962-1	Sequence 1, Appli
C 6	381.6	54.4	1767 10 US-09-884-514-1	Sequence 1, Appli
C 7	378.4	53.9	1767 10 US-09-784-962-2	Sequence 2, Appli
C 8	378.4	53.9	1767 10 US-09-884-514-2	Sequence 2, Appli
C 9	340	48.4	1768 10 US-09-784-962-3	Sequence 3, Appli
C 10	340	48.4	1768 10 US-09-784-962-4	Sequence 4, Appli
C 11	340	48.4	1768 10 US-09-884-514-3	Sequence 3, Appli
C 12	340	48.4	1768 10 US-09-884-514-4	Sequence 4, Appli
C 13	339	48.3	1768 10 US-09-884-514-6	Sequence 6, Appli
C 14	307.8	43.8	1759 10 US-09-935-428A-2	Sequence 2, Appli
C 15	273.4	38.9	7460 9 US-10-038-001-7	Sequence 7, Appli
C 16	256.4	36.5	5285 9 US-10-038-001-1	Sequence 1, Appli
C 17	256.4	36.5	5650 9 US-10-038-001-2	Sequence 2, Appli
C 18	199.4	28.4	1759 10 US-09-784-962-5	Sequence 5, Appli
C 19	199.4	28.4	1759 10 US-09-884-514-5	Sequence 5, Appli

20	42.6	6.1	592	12	US-10-042-417-31	Sequence 31, Appl
21	40.4	5.8	7869	10	US-09-954-456-1921	Sequence 1921, Ap
22	39.6	5.6	3000	9	US-10-227-353-5	Sequence 5, Appli
23	39.6	5.6	3116	9	US-09-855-754-3	Sequence 3, Appli
24	37.8	5.4	972	9	US-09-477-737-1	Sequence 1, Appli
25	37.8	5.4	1890	10	US-09-802-669-24	Sequence 24, Appl
C 26	37.8	5.4	2038	10	US-09-880-107-2102	Sequence 2102, Ap
C 27	37.8	5.4	3715	10	US-09-880-107-2300	Sequence 2300, Ap
28	37.2	5.3	1848	12	US-10-062-254-239	Sequence 239, App
29	37	5.3	2462	9	US-09-922-364A-48	Sequence 48, Appl
30	37	5.3	2462	9	US-09-254-590-48	Sequence 48, Appl
31	37	5.3	2462	9	US-10-115-695-48	Sequence 48, Appl
32	37	5.3	2462	9	US-10-116-561-48	Sequence 48, Appl
33	37	5.3	2462	9	US-10-115-671-48	Sequence 48, Appl
34	37	5.3	2462	9	US-10-115-415-48	Sequence 48, Appl
35	37	5.3	2462	9	US-10-116-260-48	Sequence 48, Appl
36	36.4	5.2	1449	9	US-09-920-671-3	Sequence 3, Appli
37	36.4	5.2	139257	9	US-09-920-671-11	Sequence 11, Appl
38	36.2	5.2	1107	10	US-09-925-300-466	Sequence 466, App
39	36.2	5.2	127197	9	US-09-754-853A-1	Sequence 1, Appli
40	36	5.1	1767	10	US-09-784-962-1	Sequence 1, Appli
41	36	5.1	1767	10	US-09-884-514-1	Sequence 1, Appli
C 42	36	5.1	2936	9	US-10-108-605-54	Sequence 54, Appl
C 43	35.8	5.1	520	9	US-10-184-644-332	Sequence 332, App
C 44	35.8	5.1	520	9	US-10-184-634-332	Sequence 332, App
45	35.6	5.1	15720	9	US-10-025-380-1058	Sequence 1058, Ap

ALIGNMENTS

RESULT 1  
US-09-935-428A-11/C  
; Sequence 11, Application US/09935428A  
; Patent No. US20020106639A1  
; GENERAL INFORMATION:  
; APPLICANT: WANG, LI  
; APPLICANT: BABIUK, LORNE A.  
; APPLICANT: POTTER, ANDREW A.  
; APPLICANT: WILLSON, PHILIP  
; TITLE OF INVENTION: POSTWEANING MULTISYSTEM WASTING SYNDROME VIRUS FROM  
; TITLE OF INVENTION: PIGS  
; FILE REFERENCE: 9000-0040  
; CURRENT APPLICATION NUMBER: US/09/935.428A  
; CURRENT FILING DATE: 2001-08-20  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/209,961  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,233  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-11  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,750  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-16  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 1768  
; TYPE: DNA  
; ORGANISM: Porcine Circovirus Type II  
US-09-935-428A-11

Query Match 88.8%; Score 623.6; DB 10; Length 1768;  
Best Local Similarity 93.0%; Pred. No. 2e-196;  
Matches 653; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy	1	ATGACGTATCCAAGGAGCGGTTACCGAAGAAGACACCGCCCGCAGCCATCTTGGC	60
Db	1735	ATGACGTATCCAAGGAGCGGTTACCGAAGAAGACACCGCCCGCAGCCATCTTGGC	1676
Qy	61	CAGATCCTCCGCGCGCCCTGGCTCGTCCACCCCGCCACCGTTACCGTGGAGAAGG	120
Db	1675	CAGATCCTCCGCGCGCCCTGGCTCGTCCACCCCGCCACCGTTACCGTGGAGAAGG	1616
Qy	121	AAATATGGCATCTTCAACACCCGCTCTCCCGCACCTTCGGATATCTGTCAAGCGAACC	180

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; PRIOR FILING DATE: 1999-07-04
; PRIOR APPLICATION NUMBER: 98 08777
; PRIOR FILING DATE: 1998-07-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Porcine circovirus
US-09-784-962-1

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	Query Match	54.4%;	Score 381.6;	DB 10;	Length 1767;
	Best Local Similarity	99.0%;	Pred. NO. 5.2e-116;		
	Matches 384;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
QY	315	CTGGCCCTGCTCCCGCATCACCCAGGGTGACAGGGAGTGGGCTCCAGTGCCTGATATTT	374		
Db	1767	CTGGCCCTGCTCCCGCATCACCCAGGGTGACAGGGAGTGGGCTCCAGTGCCTGATATCT	1708		
QY	375	AGATGATAACTTTGTAAACAAAGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTC	434		
Db	1707	AGATGATAACTTTGTAAACAAAGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTC	1648		
QY	435	CTCCCGGCATACCATAAACCCAGCCCTTCTCCTACCACCTCCCGGTACTTTACCCCCAAACC	494		
Db	1647	CTCCCGGCATACCATAAACCCAGCCCTTCTCCTACCACCTCCCGGTACTTTACCCCCAAACC	1588		
QY	495	TGTCCTAGATTTCACATATTGATTACTTCCAACCAACAACAAGAAACCCAGCTGTGGCT	554		
Db	1587	TGTCCTAGATTTCACATATTGATTACTTCCAACCAACAACAAGAAACCCAGCTGTGGCT	1528		
QY	555	GAGACTACAACCTGCTGGAAATGTAGACCACGTAGGCCCTCGGCACCTGCGTTTCGAAACACAG	614		
Db	1527	GAGACTACAACCTGCTGGAAATGTAGACCACGTAGGCCCTCGGCACCTGCGTTTCGAAACACAG	1468		
QY	615	TATATACGACCCAGGAATACAATATCCGTGTAAACCATGTATGTACAATTTCAGAGAAATTAA	674		
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QY	675	TTTTAAAGACCCCCCACTTAACCCCTTAA	702		
Db	1407	TCTTAAAGACCCCCCACTTAACCCCTTAA	1380		

## RESULT 6

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US-09-884-514-1/c
; Sequence 1, Application US/09884514
; Patent No. US20020146432A1
; GENERAL INFORMATION:
; APPLICANT: ALLAN, Gordon
; APPLICANT: MEEHAN, Brian
; APPLICANT: CLARK, Edward
; APPLICANT: HAINES, Deborah
; APPLICANT: HASSARD, Lori
; APPLICANT: HARDING, John
; APPLICANT: CHARREYRE, Catherine E.
; APPLICANT: CHAPPUIS, Gilles E.
; APPLICANT: NEWTONARDS, Francis McNeillly
; TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC
; TITLE OF INVENTION: REAGENTS
; FILE REFERENCE: ALLAN
; CURRENT APPLICATION NUMBER: US/09/884,514
; CURRENT FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: FR 9800873
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: FR 9803707
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: FR 97/12382
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 1
; LENGTH: 1767

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; TYPE: DNA
; ORGANISM: Porcine circovirus
US-09-884-514-1

Query Match      54.4%; Score 381.6; DB 10; Length 1767;
Best Local Similarity 99.0%; Pred. No. 5.2e-116;
Matches 384; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 315 CTGGCCCTGCTCCCGATCACCCAGGGTGACAGGGAGTGGGCTCCAGTGCCTGTAATTT 374
Db 1767 CTGGCCCTGCTCCCGATCACCCAGGGTGACAGGGAGTGGGCTCCAGTGCCTGTAATTC 1708

QY 375 AGATGATAACTTTGTAACAAAGGCCACAGCCCTCACCTATGACCCCTATGTAACACTACTC 434
Db 1707 AGATGATAACTTTGTAACAAAGGCCACAGCCCTCACCTATGACCCCTATGTAACACTACTC 1648

QY 435 CTCCCGCCATACCATAAACCCAGCCCTTCTCCTACCACCTCCCGGTACTTTACCCCAAAACC 494
Db 1647 CTCCCGCCATACCATAAACCCAGCCCTTCTCCTACCACCTCCCGGTACTTTACCCCAAAACC 1588

QY 495 TGTCTTAGATTTCCTACTATTGATTACTTCCAAACCAACAACAAGAAACCAAGTGTGGCT 554
Db 1587 TGTCTTAGATTTCCTACTATTGATTACTTCCAAACCAACAACAAGAAACCAAGTGTGGCT 1528

QY 555 GAGACTACAAACTGCTGGAAATGTAGACCACCGTAGGCCTCGGCACCTGCGTTCGAAACAG 614
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Db 1467 TATATACGACCGAGGAATACAATATCCCGTGTAAACCATGTATGTACAATTCAGAGAAATTTAA 1408

QY 675 TTTTAAAGACCCCTTAAACCCCTTAA 702
Db 1407 TCTTAAAGACCCCTTAAACCCCTTAA 1380

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## RESULT 7

US-09-784-962-2/c  
; Sequence 2, Application US/09784962  
; Patent No. US20020146431A1  
; GENERAL INFORMATION:  
; APPLICANT: ALLAN, Gordon M.  
; APPLICANT: MEEHAN, Brian M.  
; APPLICANT: ELLIS, John A.  
; APPLICANT: KRAKOWKA, George S.  
; APPLICANT: AUDONNET, Jean-Christophe F.  
; TITLE OF INVENTION: PORCINE CIRCOVIRUS AND PARVOVIRUS VACCINE  
; FILE REFERENCE: 454313-2338  
; CURRENT APPLICATION NUMBER: US/09/784,962  
; CURRENT FILING DATE: 2001-02-16  
; PRIOR APPLICATION NUMBER: 09/347,594  
; PRIOR FILING DATE: 1999-07-04  
; PRIOR APPLICATION NUMBER: 98 08777  
; PRIOR FILING DATE: 1998-07-06  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1767  
; TYPE: DNA  
; ORGANISM: Porcine circovirus  
US-09-784-962-2

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	Best Local Similarity	98.5%;	Pred. No. 6e-115;		
	Matches 382;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;
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Dd	1767	CTGGCCCTGCTCCCCCGATCACCCAGGGTGACAGSGAGTGGGCTCCAGTGCCTGTATTCT	1708		
QY	375	AGATGATAACTTTTGTAAACAAGGCCACAGCCCCTACACCTATGACCCCCTATGTAAACTACTC	434		







RESULT 10  
US-09-784-962-4/c  
; Sequence 4, Application US/09784962  
; Patent No. US20020146431A1  
; GENERAL INFORMATION:  
; APPLICANT: ALLAN, Gordon M.  
; APPLICANT: MEEHAN, Brian M.  
; APPLICANT: ELLIS, John A.  
; APPLICANT: KRAKOWKA, George S.  
; APPLICANT: AUDONNET, Jean-Christophe F.  
; TITLE OF INVENTION: PORCINE CIRCOVIRUS AND PARVOVIRUS VACCINE  
; FILE REFERENCE: 454313-2338  
; CURRENT APPLICATION NUMBER: US/09/784,962  
; CURRENT FILING DATE: 2001-02-16  
; PRIOR APPLICATION NUMBER: 09/347,594  
; PRIOR FILING DATE: 1999-07-04  
; PRIOR APPLICATION NUMBER: 98 08777  
; PRIOR FILING DATE: 1998-07-06  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 1768  
; TYPE: DNA  
; ORGANISM: Porcine circovirus  
US-09-784-962-4

Query Match 48.4%; Score 340; DB 10; Length 1768;  
Best Local Similarity 92.3%; Pred. No. 3.5e-102;  
Matches 358; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
QY 315 CTGGCCCTGCTCCCGCATCACCCAGGGTGACAGGGGAGTGGGCTCCAGTGGCTGTTATTTT 374  
Db 1768 CTGGCCCTGCTCCCGCATCACCCAGGGTGATAGGGGAGTGGGCTCCAGTGGCTGTTATTTT 1709  
QY 375 AGATGATAACTTTTGTAAACAAGGCCACAGCCCTCACCTATGACCCCTATGTAACTACTC 434  
Db 1708 AGATGATAACTTTTGTAAACAAGGCCACAGCCCTAACCTATGACCCCTATGTAACTACTC 1649  
QY 435 CTCCCGCCATACCATACCCAGCCCTTCTCTACCACTCCCGGTACTTTACCCCAAAACC 494  
Db 1648 CTCCCGCCATACCATACCCCAACCCTTCTCTACCACTCCCGGTACTTTACCAACCAACC 1589  
QY 495 TGTCCTAGATTCTACTATTGATTACTTCCAAACCAACAAAGAAACCAACAGCTGTGGCT 554  
Db 1588 TGTTCTTGACTCCACTATTGATTACTTCCAAACCAACAAAGAAATCAGCTTTGGCT 1529  
QY 555 GAGACTACAAACTGCTGGAAATGTAGACCACGCTAGGCCTCGGCACCTGCGTTTCGAAAACAG 614  
Db 1528 GAGACTACAAACCTCTGGAAATGTGGACCACGCTAGGCCTCGGCCTGCGTTTCGAAAACAG 1469  
QY 615 TATATACGACCAGGAATACAAATATCCGTGTACCAATGTATGTACAATTCAGAGAAATTTAA 674  
Db 1468 TAAATACGACCAGGACTACAAATATCCGTGTAAACCAATGTATGTACAATTCAGAGAAATTTAA 1409  
QY 675 TTTTAAAGACCCCCCACTTAACCCCTTAA 702  
Db 1408 TCTTAAAGACCCCCCACTTAACCCCTTAA 1381

RESULT 11  
US-09-884-514-3/c  
; Sequence 3, Application US/09884514  
; Patent No. US20020146432A1  
; GENERAL INFORMATION:  
; APPLICANT: ALLAN, Gordon  
; APPLICANT: MEEHAN, Brian  
; APPLICANT: CLARK, Edward  
; APPLICANT: HAINES, Deborah  
; APPLICANT: HASSARD, Lori  
; APPLICANT: HARDING, John  
; APPLICANT: CHARREYRE, Catherine E.

; APPLICANT: CHAPPUIS, Gilles E.  
; APPLICANT: NEWTONARDS, Francis McNeilly  
; TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC  
; FILE REFERENCE: REAGENTS  
; FILE REFERENCE: ALLAN  
; CURRENT APPLICATION NUMBER: US/09/884,514  
; CURRENT FILING DATE: 2000-06-19  
; PRIOR APPLICATION NUMBER: FR 9800873  
; PRIOR FILING DATE: 1998-01-22  
; PRIOR APPLICATION NUMBER: FR 9803707  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: FR 97/12382  
; PRIOR FILING DATE: 1997-10-03  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 1768  
; TYPE: DNA  
; ORGANISM: Porcine circovirus  
US-09-884-514-3

Query Match 48.4%; Score 340; DB 10; Length 1768;  
Best Local Similarity 92.3%; Pred. No. 3.5e-102;  
Matches 358; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
QY 315 CTGGCCCTGCTCCCGCATCACCCAGGGTGACAGGGGAGTGGGCTCCAGTGGCTGTTATTTT 374  
Db 1768 CTGGCCCTGCTCCCGCATCACCCAGGGTGATAGGGGAGTGGGCTCCAGTGGCTGTTATTTT 1709  
QY 375 AGATGATAACTTTTGTAAACAAGGCCACAGCCCTCACCTATGACCCCTATGTAACTACTC 434  
Db 1708 AGATGATAACTTTTGTAAACAAGGCCACAGCCCTAACCTATGACCCCTATGTAACTACTC 1649  
QY 435 CTCCCGCCATACCATACCCAGCCCTTCTCTACCACTCCCGGTACTTTACCCCAAAACC 494  
Db 1648 CTCCCGCCATACCAATCCCAACCCTTCTCTACCACTCCCGGTACTTTACCAACCAACC 1589  
QY 495 TGTCCTAGATTCTACTATTGATTACTTCCAAACCAACAAAGAAACCAACAGCTGTGGCT 554  
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QY 555 GAGACTACAAACTGCTGGAAATGTAGACCACGCTAGGCCTCGGCACCTGCGTTTCGAAAACAG 614  
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Db 1468 TATATACGACCAGGACTACAAATATCCGTGTAAACCAATGTATGTACAATTCAGAGAAATTTAA 1409  
QY 675 TTTTAAAGACCCCCCACTTAACCCCTTAA 702  
Db 1408 TCTTAAAGACCCCCCACTTAACCCCTTAA 1381

RESULT 12  
US-09-884-514-4/c  
; Sequence 4, Application US/09884514  
; Patent No. US20020146432A1  
; GENERAL INFORMATION:  
; APPLICANT: ALLAN, Gordon  
; APPLICANT: MEEHAN, Brian  
; APPLICANT: CLARK, Edward  
; APPLICANT: HAINES, Deborah  
; APPLICANT: HASSARD, Lori  
; APPLICANT: HARDING, John  
; APPLICANT: CHARREYRE, Catherine E.  
; APPLICANT: CHAPPUIS, Gilles E.  
; APPLICANT: NEWTONARDS, Francis McNeilly  
; TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC  
; FILE REFERENCE: REAGENTS  
; FILE REFERENCE: ALLAN  
; CURRENT APPLICATION NUMBER: US/09/884,514  
; CURRENT FILING DATE: 2000-06-19

Db 1707 AGATGATAACTTTGTAAACAAGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTC 1648  
QY 435 CTCCCGCCATACCATAAACCAGCCCTTCTCTACCACTCCCGGTACTTTACCCCAACC 494  
Db 1647 CTCCCGCCATACCATAAACCAGCCCTTCTCTACCACTCCCGTACTTTACCCCAACC 1588  
QY 495 TGTCTAGATTTCACCTATTGATTACTTCCAACCAACAACAAGAAACAGCTGTGGCT 554  
Db 1587 TGTCTAGATTCCACTATTGATTACTTCCAACCAACAACAAGAAATCAGCTGTGGCT 1528  
QY 555 GAGACTACAAACTGCTGGAATGTAGACCACGTAGGCCTCGGCACCTGCGTTCGAAAACAG 614  
Db 1527 GAGACTACAAACTACTGGAATGTAGACCACGTAGGCCTCGGCACCTGCGTTCGAAAACAG 1468  
QY 615 TATATACGACGAGGAATACAATATCCGTGTAACCATGTATGTACAATTTCAGAGAATTAA 674  
Db 1467 TATATACGACGAGGAATACAATATCCGTGTAACCATGTATGTACAATTTCAGAGAATTAA 1408  
QY 675 TTTTAAAGACCCCCCACTTAACCCCTTAA 702  
Db 1407 TCTTAAAGACCCCCCACTTAACCCCTTAA 1380

RESULT 8

US-09-884-514-2/c  
; Sequence 2, Application US/09884514  
; Patent No. US20020146432A1  
; GENERAL INFORMATION:  
; APPLICANT: ALLAN, Gordon  
; APPLICANT: MEEHAN, Brian  
; APPLICANT: CLARK, Edward  
; APPLICANT: HAINES, Deborah  
; APPLICANT: HASSARD, Lori  
; APPLICANT: HARDING, John  
; APPLICANT: CHARREYRE, Catherine E.  
; APPLICANT: CHAPPUIS, Gilles E.  
; APPLICANT: NEWTONARDS, Francis McNeilly  
; TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC  
; TITLE OF INVENTION: REAGENTS  
; FILE REFERENCE: ALLAN  
; CURRENT APPLICATION NUMBER: US/09/884,514  
; CURRENT FILING DATE: 2000-06-19  
; PRIOR APPLICATION NUMBER: FR 9800873  
; PRIOR FILING DATE: 1998-01-22  
; PRIOR APPLICATION NUMBER: FR 9803707  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: FR 97/12382  
; PRIOR FILING DATE: 1997-10-03  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1767  
; TYPE: DNA  
; ORGANISM: Porcine circovirus  
US-09-884-514-2

Query Match 53.9%; Score 378.4; DB 10; Length 1767;  
Best Local Similarity 98.5%; Pred. No. 6e-115;  
Matches 382; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 315 CTGGCCCTGCTCCCGGATCACCCAGGGTGACAGGGGAGTGGGCTCCAGTGTATTATTT 374  
Db 1767 CTGGCCCTGCTCCCGGATCACCCAGGGTGACAGGGGAGTGGGCTCCAGTGTATTATTT 1708  
QY 375 AGATGATAACTTTGTAAACAAGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTC 434  
Db 1707 AGATGATAACTTTGTAAACAAGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTC 1648  
QY 435 CTCCCGCCATACCATAAACCAGCCCTTCTCTACCACTCCCGGTACTTTACCCCAACC 494  
Db 1647 CTCCCGCCATACCATAAACCAGCCCTTCTCTACCACTCCCGTACTTTACCCCAACC 1588  
QY 495 TGTCTAGATTTCACCTATTGATTACTTCCAACCAACAACAAGAAACAGCTGTGGCT 554

Db 1587 TGTCTAGATTCCACTATTGATTACTTCCAACCAACAACAAGAAATCAGCTGTGGCT 1528  
QY 555 GAGACTACAAACTGCTGGAATGTAGACCACGTAGGCCTCGGCACCTGCGTTCGAAAACAG 614  
Db 1527 GAGACTACAAACTACTGGAATGTAGACCACGTAGGCCTCGGCACCTGCGTTCGAAAACAG 1468  
QY 615 TATATACGACGAGGAATACAATATCCGTGTAACCATGTATGTACAATTTCAGAGAATTAA 674  
Db 1467 TATATACGACGAGGAATACAATATCCGTGTAACCATGTATGTACAATTTCAGAGAATTAA 1408  
QY 675 TTTTAAAGACCCCCCACTTAACCCCTTAA 702  
Db 1407 TCTTAAAGACCCCCCACTTAACCCCTTAA 1380

RESULT 9

US-09-784-962-3/c  
; Sequence 3, Application US/09784962  
; Patent No. US20020146431A1  
; GENERAL INFORMATION:  
; APPLICANT: ALLAN, Gordon M.  
; APPLICANT: MEEHAN, Brian M.  
; APPLICANT: ELLIS, John A.  
; APPLICANT: KRAKOWKA, George S.  
; APPLICANT: AUDONNET, Jean-Christophe F.  
; TITLE OF INVENTION: PORCINE CIRCOVIRUS AND PARVOVIRUS VACCINE  
; FILE REFERENCE: 454313-2338  
; CURRENT APPLICATION NUMBER: US/09/784,962  
; CURRENT FILING DATE: 2001-02-16  
; PRIOR APPLICATION NUMBER: 09/347,594  
; PRIOR FILING DATE: 1999-07-04  
; PRIOR APPLICATION NUMBER: 98 08777  
; PRIOR FILING DATE: 1998-07-06  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 1768  
; TYPE: DNA  
; ORGANISM: Porcine circovirus  
US-09-784-962-3

Query Match 48.4%; Score 340; DB 10; Length 1768;  
Best Local Similarity 92.3%; Pred. No. 3.5e-102;  
Matches 358; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
QY 315 CTGGCCCTGCTCCCGGATCACCCAGGGTGACAGGGGAGTGGGCTCCAGTGTATTATTT 374  
Db 1768 CTGGCCCTGCTCCCGGATCACCCAGGGTGATAGGGGAGTGGGCTCCAGTGTATTATTT 1709  
QY 375 AGATGATAACTTTGTAAACAAGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTC 434  
Db 1708 AGATGATAACTTTGTAAACAAGGCCACAGCCCTTAACCTATGACCCCATATGTAAACTACTC 1649  
QY 435 CTCCCGCCATACCATAAACCAGCCCTTCTCTACCACTCCCGGTACTTTACCCCAACC 494  
Db 1648 CTCCCGCCATACAATCCCCCAACCCCTTCTCTACCACTCCCGTACTTTCACACCCCAACC 1589  
QY 495 TGTCTAGATTTCACCTATTGATTACTTCCAACCAACAACAAGAAACAGCTGTGGCT 554  
Db 1588 TGTCTTAGACTCCACTATTGATTACTTCCAACCAACAACAAGGAATCAGCTTTGGCT 1529  
QY 555 GAGACTACAAACTGCTGGAATGTAGACCACGTAGGCCTCGGCACCTGCGTTCGAAAACAG 614  
Db 1528 GAGGCTACAAACCTCTAGAAATGTGGACCACAGTAGGCCTCGGCACCTGCGTTCGAAAACAG 1469  
QY 615 TATATACGACGAGGAATACAATATCCGTGTAACCATGTATGTACAATTTCAGAGAATTAA 674  
Db 1468 TATATACGACGAGGACTACAATATCCGTGTAACCATGTATGTACAATTTCAGAGAATTAA 1409  
QY 675 TTTTAAAGACCCCCCACTTAACCCCTTAA 702  
Db 1408 TCTTAAAGACCCCCCACTTAACCCCTTAA 1381

Best Local Similarity 67.0%; Pred. NO. 1.7e-91;										
Matches 470; Conservative 0; Mismatches 222; Indels 9; Gaps 2;										
QY	1	ATGACGTATCC	AAGGAGCGG	TTACCGAAGA	AAGACACCG	CCCCCGG	CAGCCATCTT	GGC	60	
Db	1723	ATGACGTGGC	CAAGGAGCG	TTACCGCAGA	AGAGGACCG	CCCCCGG	CAGCCATCTT	GGA	1664	
QY	61	CAGATCCTCC	GGCGCGCC	CTGGCTCG	TCTCCACCC	-----	CCGCCACCG	TTACCGCTGG	114	
Db	1663	AACATCCTCC	GGAGAAGAC	CCATATTT	TGGCACAC	CCCGCCCT	TCAGAAAC	CGTTACAGATGG	1604	
QY	115	AGAAGGAAAA	ATGGCATCT	TTCAACAC	CCCGCCTCT	CCCGCACCT	TTCGGATATA	CTGTCAAG	174	
Db	1603	CGCCGAAAG	ACGGGTATCT	TCAATTCC	CGCCTTCT	TACAGAAT	TTGTACTC	CACCAATAA	1544	
QY	175	CGAACCA	CAGTCAGAAC	CCCTCCT	CTGGGGGT	GGACATGAT	GAGATTCA	ATATAATGAC	234	
Db	1543	GGA---	GGATACTCG	CAGCCATCT	TGGAATGT	TAACTACCT	CAAAATTC	AACATCGGCCAG	1487	
QY	235	TTTCTTCCC	CCAGGAGGG	GGGTCAAA	CCCCCGCTCT	GTGCCCTTT	TGAATACT	ACACAAATA	294	
Db	1486	TTCTTCCCC	CTCAGGGG	CACCAAC	CCCCCTAC	CCCTTACCT	TTCCAAT	TACTACCGTATT	1427	
QY	295	AGAAAGG	TTAAGTTGA	ATTCTGG	CCCTCTCT	CCCCGATCA	CCCCAGGGT	GACAGGGAGTG	354	
Db	1426	AGAAAGG	CTAAATATGA	ATTTTAC	CCCCAGAG	ACCCATCAC	CTCTAAT	CAAAAGAGGTGT	1367	
QY	355	GGCTCCAG	TGCTGTTAT	TTTAGATG	ATAACTTT	TGTAACAA	AGGCCAC	AGCCCTCACCTAT	414	
Db	1366	GGTCCACT	GTTGTTATCT	TGGATGCC	AACCTTGT	TAACCCCTC	CAACCACT	TGGCCTAT	1307	
QY	415	GACCCCTAT	GTAAACTACT	CTCTCC	CGCCATACC	ATAACCC	AGCCCTTCT	CTTACCACTCC	474	
Db	1306	GACCCCTAT	ATAACTACT	CTCTCC	CGCCACAC	CAATAAGG	CAGCCCTTT	ACCTACCACTCC	1247	
QY	475	CGTACTTTA	CCCCCAAC	CTGTCT	CCTAGATT	TTCACTATT	GATTGATT	TTCCAAACCAACAAC	534	
Db	1246	AGGTACTTC	ACCCCAAC	CTGAGCT	GGACCA	AAACAAT	TGATTGGT	TCCACCAACAATAAT	1187	
QY	535	AAAAGAA	ACCAGCTGT	GGTGAG	ACTACAA	ACTGCTG	GGAATGT	AGACCACGTAGGCCCTC	594	
Db	1186	AAAAGAA	ACCAGCTGT	GGTCCAT	TTTAAAT	ATACCC	ACACCAAT	GTGAGGCACACAGGCCCTC	1127	
QY	595	GGCACTG	CGTTTCA	AAAAAC	AGTATATA	ACGACC	AGGAATACA	ATATCCGTTGTA	ACCATGTAT	654
Db	1126	GGCTATG	CGCTCCA	AAATGC	AGCCAC	AGCCCA	AAAAAT	TATGTGGTA	AGGCTGACTATTAT	1067
QY	655	GTACAATT	CAGAGAAT	TTTAA	TTTAA	AGACCC	CCCCACTTAA	695		
Db	1066	GTACAATT	CAGAGAAT	TTTAT	CTCTAA	AAGAC	CCCTCTAA	ATAA 1026		

RESULT 15  
US-10-038-001-7/c  
; Sequence 7, Application US/10038001  
; Publication No. US20020187952A1  
; GENERAL INFORMATION:  
; APPLICANT: PALMER, Kenneth E.  
; APPLICANT: POGUE, Gregory P.  
; APPLICANT: MCCORMICK, Alison  
; TITLE OF INVENTION: ROLLING CIRCLE REPLICON EXPRESSION  
; TITLE OF INVENTION: VECTORS  
; FILE REFERENCE: 008010179CPUS01  
; CURRENT APPLICATION NUMBER: US/10/038,001  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 09/505,477  
; PRIOR FILING DATE: 2000-02-16  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 7460  
; TYPE: DNA  
; ORGANISM: Porcine circovirus

US-10-038-001-7									
Query Match 38.9%; Score 273.4; DB 9; Length 7460;									
Best Local Similarity 68.4%; Pred. No. 1.1e-79;									
Matches 411; Conservative 0; Mismatches 181; Indels 9; Gaps 2;									
QY	1	ATGACGTAT	CCAAGGAGG	CGGCTT	ACCGAAGA	AGACAC	CGCCCCCGG	CAGCCATCTT	GGC 60
Db	602	ATGACGTGG	CCCAAGAGG	CGGCTT	ACCGCAGA	AGAGAGG	ACCGCCCCCGG	CAGCCATCTT	GGG 543
QY	61	CAGATCCTC	CGCGCGCC	CTGGCTCG	TCCACCC-----	CCGCCACCG	TTACCGCTGG	114	
Db	542	AACATCCTC	CGCAGAAG	ACCATATT	TGGCACAC	CCCCCGCTT	CAGAAACCG	TTACAGATGG	483
QY	115	AGAAGGAAA	AAATGGCAT	CTTCAAC	ACCGCCCTCT	CCCGCACCT	TTCCGATATAC	TGTCAAG	174
Db	482	CGCCGAAA	AGAGGGTAT	CTTCAATT	CGCGCTTCT	TAGAGAAT	TTGTACTC	ACCATAGAA	423
QY	175	CGAACCA	CAGTCAGAAC	CGCCCTC	CTGGCGGTG	GACATGAT	GAGATTCA	ATATTAATGAC	234
Db	422	GGA---	GGACACTCG	CAGCCATCT	TGGAATGT	TAAACAGCT	CAGATTCA	ACATCGGCCAG	366
QY	235	TTTCTTCCC	CCAGGAGG	GGGTCAAA	CCCCCGCTCT	GTGCCCTTT	GAAATACT	ACAGAAATA	294
Db	365	TTCTCCCCC	CTCAGGCG	GCACCA	ACCCCTTAC	CCCTTAC	CTTCCAAT	TACTACCGTATT	306
QY	295	AGAAAGG	TTAAGGTTGA	ATTCTGG	CCCTGTCT	CCCGGATCA	CCCGGGT	GACAGGGAGTG	354
Db	305	AGAAAGG	CTAAATATGA	ATTTTAC	CCCGAGAG	ACCCCATCAC	CTCTAAT	CAAAAGAGGTGT	246
QY	355	GGCTCCAG	TGCTGTTATT	TTTAGATG	ATAACTTT	TGTAACAA	AGGCCAC	AGCCCTCACCTAT	414
Db	245	GGGTCCACT	GCTGTTATCT	TGGATGCC	AACTTTGT	AACCCCTC	CAACCACT	TGGCCCTAT	186
QY	415	GACCCCTAT	GTAAACTACT	CTCTCC	CGCCATACC	ATAACCC	AGCCCTTCT	CTTACCCTCC	474
Db	185	GACCCCTAT	ATAACTACT	CTCTCC	CGCCAC	ACCATAA	AGGCAGC	CCCTTTACCTACCACTCC	126
QY	475	CGTACTTTA	CCCCCAAC	CTGTCT	AGATTTC	ACTATTG	ATTGATTACT	TTCCAAACCAACAAC	534
Db	125	AGGTACTTT	CACCCCCA	AACTGAG	CTGGAC	CAACAA	ATTTGATTGG	TTCCAGCCCAATAAT	66
QY	535	AAAAGAA	ACCAGCTGT	GGTGAG	ACTACAA	AACTGCTG	GGAATGT	AGACCACGTAGGCCCTC	594
Db	65	AAAAGAA	ACCAGCTGT	GGCTCCA	TTTAAAT	TACCCAC	ACCAATGT	TCGACCACACAGGCCCTA	6
QY	595	G 595							
Db	5	G 5							

Search completed: May 18, 2003, 13:00:07  
Job time : 170 secs

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; PRIOR APPLICATION NUMBER: FR 9800873
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: FR 9803707
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: FR 97/12382
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1768
; TYPE: DNA
; ORGANISM: Porcine circovirus
US-09-884-514-4

Query Match      48.4%; Score 340; DB 10; Length 1768;
Best Local Similarity 92.3%; Pred. No. 3.5e-102;
Matches 358; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 315 CTGGCCCTGCTCCCGATCACCCAGGGTGACAGGGGAGTGGGCTCCAGTGGCTGTTATTTT 374
Db 1768 CTGGCCCTGCTCCCGCATCACCCAGGGTGATAGGGGAGTGGGCTCCACTGCTGTTATTTCT 1709

QY 375 AGATGATAACTTTGTAAAGAGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTC 434
Db 1708 AGATGATAACTTTGTAAAGAGCCACAGCCCTAACCTATGACCCCATATGTAAACTACTC 1649

QY 435 CTCCCGCCATACCATACCCAGCCCTTCTCCTACCACTCCCGGTACTTTACCCCAAAACC 494
Db 1648 CTCCCGCCATACCAATCCCCCAACCTTCTCCTACCACTCCCGTTACTTCACACCCAAACC 1589

QY 495 TGTCTAGATTTCACATATTGATTACTTCCAACCAACAAACAAAGAAACCAAGCTGTGGCT 554
Db 1588 TGTCTTGACTCCACATATTGATTACTTCCAACCAACAAACAAAGGAATCAGCTTTGGCT 1529

QY 555 GAGACTACAAACTGCTGGAATGTAGACCAAGTAGGCTCGGCACCTGCGTTTCGAAACAG 614
Db 1528 GAGACTACAAACCTCTGGAATGTGACCAAGTAGGCTCGGCACCTGCGTTTCGAAACAG 1469

QY 615 TATATACGACCAAGGATACAAATATCCGTGTAAACCAATGTATGATGATGATGATGATGAT 674
Db 1468 TAAATACGACCAAGGACTACAAATATCCGTGTAAACCAATGTATGATGATGATGATGATGAT 1409

QY 675 TTTTAAAGACCCCTTAAACCTTAA 702
Db 1408 TCTTAAAGACCCCTTAAACCTTAA 1381
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RESULT 13
US-09-884-514-6/c
; Sequence 6, Application US/09884514
; Patent No. US20020146432A1
; GENERAL INFORMATION:
; APPLICANT: ALLAN, Gordon
; APPLICANT: MEEHAN, Brian
; APPLICANT: CLARK, Edward
; APPLICANT: HAINES, Deborah
; APPLICANT: HASSARD, Lori
; APPLICANT: HARDING, John
; APPLICANT: CHARREYRE, Catherine E.
; APPLICANT: CHAPPUIS, Gilles E.
; APPLICANT: NEWTONARDS, Francis McNeilly
; TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC
; TITLE OF INVENTION: REAGENTS
; FILE REFERENCE: ALLAN
; CURRENT APPLICATION NUMBER: US/09/884,514
; CURRENT FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: FR 9800873
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: FR 9803707
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: FR 97/12382
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 6
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1768
; TYPE: DNA
; ORGANISM: Porcine circovirus
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)..(1768)
; OTHER INFORMATION: N represents A or C or G or T
US-09-884-514-6

Query Match      48.3%; Score 339; DB 10; Length 1768;
Best Local Similarity 92.2%; Pred. No. 7.5e-102;
Matches 357; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 316 TGGCCCTGCTCCCGATCACCCAGGGTGACAGGGGAGTGGGCTCCAGTCCAGTGGCTTATTTA 375
Db 1768 TGGCCCTGCTCCCGCATCACCCAGGGTGATAGGGGAGTGGGCTCCACTGCTGTTATTTCTA 1709

QY 376 GATGATAACTTTGTAAACAAAGGCCACAGCCCTCACCTATGACCCCTATGTAAACTACTCC 435
Db 1708 GATGATAACTTTGTAAACAAAGGCCACAGCCCTAACCTATGACCCCATATGTAAACTACTCC 1649

QY 436 TCCCGCCATACCATACCCAGCCCTTCTCCTACCACTCCCGGTACTTTACCCCAACCT 495
Db 1648 TCCCGCCATACCAATCCCCCAACCTTCTCCTACCACTCCCGTTACTTCACACCCCAACCT 1589

QY 496 GTCCTAGATTTCACATATTGATTACTTCCAAACCAACAAACAAAGAAACCAAGCTGTGGCTG 555
Db 1588 GTTCTTGACTCCACTATTGATTACTTCCAAACCAACAAAGGAATCAGCTTTGGCTG 1529

QY 556 AGACTACAAACTGCTGGAATGTAGACACAGTAGGCTCGGCACCTGCGTTTCGAAACAGT 615
Db 1528 AGGCTACAAACCTCTAGAAATGTGGACACAGTAGGCTCGGCACCTGCGTTTCGAAACAGT 1469

QY 616 ATATACGACCAAGGATACAAATATCCGTGTAAACCAATGTATGATGATGATGATGATGAT 675
Db 1468 ATATACGACCAAGGACTACAAATATCCGTGTAAACCAATGTATGATGATGATGATGATGAT 1409

QY 676 TTTTAAAGACCCCTTAAACCTTAA 702
Db 1408 CTTAAAGACCCCTTAAACCTTAA 1382
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RESULT 14
US-09-935-428A-2/c
; Sequence 2, Application US/09935428A
; Patent No. US20020106639A1
; GENERAL INFORMATION:
; APPLICANT: WANG, LI
; APPLICANT: BABIUK, LORNE A.
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: WILSON, PHILIP
; TITLE OF INVENTION: POSTWEANING MULTISYSTEM WASTING SYNDROME VIRUS FROM
; TITLE OF INVENTION: PIGS
; FILE REFERENCE: 9000-0040
; CURRENT APPLICATION NUMBER: US/09/935,428A
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/209,961
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,233
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,750
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1759
; TYPE: DNA
; ORGANISM: Porcine Circovirus Type I
US-09-935-428A-2

Query Match      43.8%; Score 307.8; DB 10; Length 1759;
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